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| <p>(54) Title: NUCLEIC ACID MOLECULES ASSOCIATED WITH MELANOMA AND THYROID TUMORS</p> | | |
| <p>(57) Abstract The present invention relates to isolated nucleic acid molecules associated with melanoma or thyroid tumors and compositions derived therefrom. The present invention further relates to methods for diagnosing and treating melanoma, thyroid tumors and other related pathological conditions such as rectal cancer, lung cancer, breast cancer and colon cancer, by employing such nucleic acid molecules and compositions.</p> | | |

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NUCLEIC ACID MOLECULES ASSOCIATED
WITH MELANOMA AND THYROID TUMORS

FIELD OF THE INVENTION

5 This invention relates to isolated nucleic acid molecules associated with melanoma and thyroid tumors as well as uses thereof for diagnosing and treating melanoma and thyroid tumors.

10 **BACKGROUND OF THE INVENTION**

 Recent advances in the understanding of the molecular mechanisms of antigen recognition have led to many novel immunotherapy approaches for the treatment of human cancer. One approach is by stimulating a patient's immune system with antigens that are specifically expressed by cancerous cells, i.e., tumor vaccines. Specific tumor vaccines require pre-identification of tumor associated antigens, i.e., molecules that are either specifically expressed or overexpressed in tumor cells.

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 Extensive efforts have been made to identify tumor associated antigens in humans by using two approaches which are referred to as the genetic approach and the biochemical approach. The genetic approach is exemplified by dePlaen et al., *Proc. Natl. Sci. USA* 85: 2275 (1988), incorporated herein by reference. In this approach, cDNA libraries prepared from antigen-positive tumor-cell lines are transfected into antigen-negative recipient cells, such as COS cells or variants of tumor cell lines. The transfectants are subsequently screened for the expression of tumor antigens which are recognized by tumor-specific cytolytic T-Lymphocyte clones ("CTLs"). The biochemical approach, exemplified by Mandelblom et

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30

al. *Nature* 369: 69 (1994) which is incorporated herein by reference, is based on acidic elution of peptides which are bound to MHC-class I molecules at the surface of tumor cells. Such elution produces
5 pools of peptides which are subsequently fractionated by reverse-phase high performance liquid chromatography (HPLC). Tumor specific antigenic peptides are subsequently identified based on their ability to activate tumor-specific CTL clones.

10 Application of these two approaches has led to the molecular identification of new human antigens in human tumors, most notably in malignant melanoma, such as MAGE-1, Tyrosinase and MART-1. See, e.g., van der Bruggen et al., *Science* 254: 1643-1647 (1991);
15 Brichard et al., *J. Exp. Med.* 178: 489-495 (1993); Kawakami et al., *Proc. Natl. Acad. Sci. USA* 91: 3515-3519; Cox et al., *Science* 264: 716-719 (1994).

However, these two approaches have the following disadvantages. First, such methods are
20 enormously cumbersome, time-consuming and expensive. Second, these methods depend on the establishment of autologous tumor cells in culture and isolation of stable autologous CTL clones that recognize antigens on the cultured tumor cells. It is difficult to establish
25 cell lines from certain types of tumors, as shown by, e.g., Oettgen, et al., *Immunol. Allerg. Clin. North. Am.* 10:607-637 (1990). In addition, malignant cell lines established from a patient which are capable of growing *in vitro* may not express the complete spectrum
30 of tumor associated antigens of the patient's original tumor. It is also known that some epithelial cell type cancers are poorly susceptible to CTLs *in vitro*, precluding routine analysis. Third, the relevance of

an identified tumor associated antigen to the
respective tumor *in vivo* remains to be proven, as the
respective CTLs can be obtained not only from patients
with the respective tumor, but also from healthy
5 individuals.

These problems have stimulated the art to
develop alternative methodologies. One such
methodology is described by Sahin et al., *Proc. Natl.*
Acad. Sci. USA 92: 11810-11913 (1995), incorporated
10 herein by reference. Also, see U.S. Patent No.
5,698,396 and International Application WO 96/40209,
both of which are incorporated herein by reference.
According to this method, a cDNA library is prepared
from a pathological sample of a patient, e.g., tumor
15 cells. The library is expressed in host cells, and
screened with diluted serum from a patient which has
been pre-treated to remove interfering binding
partners. Host cells expressing the antigens are
identified by their strong reactivity toward the
20 antibodies in the serum in a binding assay. This
method is also known as the SEREX method ("Serological
Identification of Antigens by Recombinant Expression
Cloning").

Application of the SEREX methodology has
25 confirmed the expression of previously identified tumor
associated antigens that are associated with melanoma,
renal cell carcinoma and Hodgkins' disease.
Application of the SEREX methodology has also led to
the identification of novel genes encoding tumor-
30 associated antigens, such as HOM-RCC-3.11, HOM-HD-21
and NY-ESO-1. See Sahin et al. (1995); Türeci et al.
(1997a), *J. Biol. Chem.* 272: 6416- 6422; Crew et al.
(1995), *EMBO J.* 144: 2333-2340; Chen et al. (1997),

Proc Natl. Acad. Sci. USA 94: 1914-1918, review by Türeci et al. (1997b) *Molecular Medicine Today* 3(8): 342-349 and review by Sahin et al. (1997) *Current Opinion in Immunology* 9: 709-716 . Since the

5 molecular identification of immunogenic proteins by the SEREX methodology is based on the reactivity of such proteins with patients' sera, immunogenic proteins which can be identified by SEREX are not restricted to cell-surface antigens and include a more complete

10 repertoire of proteins expressed by a tumor. In fact, the SEREX methodology permits the identification of proteins which are abnormally expressed by cells of any pathological condition that are capable of eliciting a strong antibody immune response in the patient.

15 The antigens identified by SEREX can be classified into different categories based on the expression patterns of these antigens, as described by Türeci et al. (1997b), *Molecular Medicine Today* 3(8): 342- 349. One category of the SEREX-detected antigens

20 are tumor-specific antigens derived from transcriptionally activated genes which are not expressed in normal tissues, such as HOM-MEL-40. Another category of the SEREX-detected antigens are differentiation antigens which are expressed in tumor

25 cells as well as in normal cells developed from the same precursor origin, e.g., Tyrosinase. Yet another category of the SEREX-detected antigens are derived from mutated genes, such as a mutated tumor suppressor gene p53. Still another category of the SEREX-detected

30 antigens are products of alternative splicing, e.g., the splice variant of restin (associated with Hodgkin's disease). The majority of the SEREX-detected antigens

are encoded by genes which are expressed in normal tissues and are overexpressed in tumors, e.g., HOM-HD-21 (associated with Hodgkin's disease) and carbonic anhydrase (associated with renal cancer). SEREX has also identified antigens encoded by genes which are expressed at similar levels in normal tissues and in tumors, such as CCAAT enhancer-binding protein HOM-MEL-2.4. It is proposed that this category of tumor associated antigens are detected by SEREX perhaps due to unusual protein processing, and therefore, unusual presentation of antigens in tumors. SEREX has also identified non-cancer-related autoantigens involved in, e.g., autoimmune diseases, such as NY-ESO-2' (encoding U1 snRNP).

In accordance with the present invention, the SEREX methodology has been applied to melanoma samples and thyroid tumor samples. A number of nucleic acid molecules have been isolated and sequenced. These results are the subject of this invention, which are elaborated upon the disclosure which follows.

SUMMARY OF THE INVENTION

The present invention is directed to isolation and identification of nucleic acid molecules which are associated with melanoma and thyroid tumors. In particular, ten nucleic acid molecules have been isolated by applying the SEREX methodology to melanoma samples, and ten nucleic acid molecules have been isolated by applying the SEREX methodology to thyroid tumor samples.

Accordingly, one embodiment of the present invention is directed to newly isolated nucleic acid

molecules, MEL 3, MEL7, Thy5, Thy6, Thy 11, Thy14 and Thy 15 (SEQ ID NOS: 3, 7, 14, 15, 17 and 19-20). The present invention also contemplates nucleic acid molecules, the complement sequences of which hybridize under stringent conditions to at least one of SEQ ID NOS: 3, 7, 14, 15, 17 and 19-20.

The present invention further contemplates vectors containing any one of the above nucleic acid molecules, as well as host cells transformed with such vectors. In a preferred embodiment, the present invention provides an antigen presenting cell transformed with one of such expression vectors, having an HLA/peptide complex at the cell surface.

In another embodiment, the present invention provides proteins encoded by the nucleic acid molecules of SEQ ID NOS: 3, 7, 14, 15, 17 and 19-20 or parts thereof.

Still another embodiment of the present invention provides antibodies directed towards a protein encoded by any one of the nucleic acid molecules of SEQ ID NOS: 3, 7, 14, 15, 17 and 19-20 or parts thereof.

The present invention is also directed to isolated HLA/peptide complexes, wherein the peptide is encoded by a fragment of any one of the nucleic acid molecules of SEQ ID NOS: 3, 7, 14, 15, 17 and 19-20.

A further aspect of the present invention is directed to methods for diagnosing pathological conditions characterized by an abnormal expression of at least one of the nucleic acid molecules encompassing SEQ ID NOS: 1-20. The pathological condition includes melanoma, the presence of a thyroid tumor, rectal

cancer, lung cancer, breast cancer or colon cancer. According to the present invention, the determination of the abnormal expression of a nucleic acid molecule can be made by assaying a component manifesting the expression of such molecule, such as mRNA, protein(s),
5 antibodies in the serum, presence of specific CTLs, or cells presenting an antigenic peptide.

Another aspect of the present invention is directed to pharmaceutical compositions. The
10 pharmaceutical compositions of the present invention can include an antisense molecule of one or more of the nucleic acid molecules encompassing any one of SEQ ID NOS: 1-20, a protein encoded by a nucleic acid molecule encompassing any one of SEQ ID NOS: 1-20 or parts of
15 such protein, an antibody directed to such a protein, a cell presenting an antigenic peptide at the surface, a CTL generated ex vivo against such cell, or combinations thereof.

The subject therapeutic compositions of the
20 present invention may be administered to a subject for treating a pathological condition in the subject, which is characterized by an abnormal expression of at least one of the nucleic acid molecules encompassing SEQ ID NOS: 1-20. Accordingly, methods of treatment are also
25 provided by the present invention.

DETAILED DESCRIPTION OF THE INVENTION

The present invention relates to isolated nucleic acid molecules that are associated with
30 melanoma or thyroid tumors. The present invention further relates to proteins encoded by such nucleic acid molecules, antibodies directed against such proteins and cells expressing such nucleic acid

molecules. The present invention also provides pharmaceutical compositions as well as methods for diagnosing and treating melanoma, thyroid tumors and other related pathological conditions.

5 Nucleic acid molecules encoding tumor associated antigens have been identified by employing the SEREX methodology as described by Sahin et al. (1995). According to SEREX, samples of suspected abnormality, e.g., tumor cells, can be obtained from
10 patients via routine clinical procedures. RNAs are purified from the freshly isolated samples for preparing a cDNA library, which is subsequently cloned into an appropriate expression vector. The choice of vectors may vary, depending on the host cells. When
15 the host cell is a eukaryotic cell, yeast, viral or baculoviral vectors are preferred. When the host cell is a prokaryotic cell, then phage vectors are preferred, such as a λ phage vector. The resulting vector-carried library is then transformed into a host
20 cell. The skilled artisan is familiar with the choice of host cells, including bacteria cells such as strains of *E. coli*, strains of *Pseudomonas* such as *Pseudomonas aeruginosa* or strains of *Bacillus*, yeast cells such as strains of *Saccharomyces* or *Pichia pastoris*, CHO cells
25 such as CHO-1, COS cells such as COS-7 and insect host cells such as *Spodoptera frugiperda*. Once the host cells receive the vectors, the cells are cultivated and induced so as to express the proteins encoded by the nucleic acid molecules of the cDNA library.

30 The expressed proteins as well as derivatives thereof, such as posttranslationally-modified products (e.g., glycoproteins or lipoproteins) and polypeptide or peptide fragments processed therefrom, are then

contacted with a sample secured from a patient for identifying the clones of interest. A preferred sample is the patient's body fluid, such as serum. The serum may be obtained via routine clinical procedures from both autologous and non-autologous patients afflicted with the relevant pathological condition such as a tumor. Such serum is treated prior to use in order to remove components in the serum which recognize either the host cell or molecules derived from the vector other than the specific target molecule. Such pretreatment procedure is described by, e.g., Sahin et al. (1995).

When the expressed proteins and derivatives thereof are contacted with the pretreated patient's sample, the immune components present in the patient's sample, e.g., IgG, which are specific for a protein or derivative thereof will bind thereto. Preferably, the proteins and derivatives can be immobilized to a solid material, e.g., nitrocellulose, to facilitate the binding. The binding can be detected by a variety of assays, for example, assays using anti-human IgG conjugated with an identifiable label, such as an enzyme, a dye, or a radiolabel. Once positive clones are identified, i.e., clones expressing proteins or derivatives which are bound by the immune components from the patient's sample, the corresponding cDNA can be isolated and sequenced via routine procedures.

The SEREX methodology permits the identification of not only cell surface antigens, but any molecules which are abnormally expressed by cells that are capable of eliciting a strong antibody immune response in the patient. See, e.g., Türeci et al. (1997b).

By applying the SEREX methodology to human melanoma samples and thyroid tumor samples, the present invention provides the isolation and identification of nucleic acid molecules associated with melanoma (MEL 1-10) and nucleic acid molecules associated with thyroid tumors (Thy 1-3, 5-6, 9, 11-12 and 14-15), respectively (SEQ ID NOS: 1-20). These nucleic acid molecules have been compared with sequences in the databases and are resolved into both known and unknown sequences. Table II summarizes the results. Whether previously known or unknown, these isolated nucleic acid molecules have been identified by the instant invention to be associated with either melanoma or thyroid tumors.

Accordingly, one embodiment of the present invention is directed to newly isolated nucleic acid molecules that are associated with melanoma (MEL3 and MEL7) or thyroid tumors (Thy 5-6, 11 and 14-15). In particular, the present invention contemplates isolated nucleic acid molecules having a sequence as set forth in any one of SEQ ID NOS: 3, 7, 14-15, 17 and 19-20.

The term "associated" or "association" is used herein to indicate that a relevant nucleic acid molecule is abnormally expressed in melanoma or thyroid tumors. These nucleic acid molecules may also be expressed by cells other than melanoma cells or thyroid tumor cells, e.g., cells of other types of tumors, or cells of other disorders such as an autoimmune disorder. For example, the present invention has also shown that the isolated nucleic acid molecules scored positive in the SEREX screening assay using sera from patients having rectal, lung, breast or colon cancer, indicating that an abnormal expression of these nucleic

acid molecules is also present in rectal, lung, breast or colon cancer.

5 The term "abnormal expression" as used herein refers to an expression that is not present in normal cells or an expression that is present in normal cells at a lower level. In the present invention, "an abnormal expression" can also be used to refer to an unusual processing of the protein expressed from a nucleic acid, which is not present in normal cells and
10 which results in unusual presentation of antigenic peptides at the cell surface.

 Another embodiment of the present invention is directed to nucleic acid molecules, the complement sequences of which hybridize under stringent conditions
15 to any one of SEQ ID NOS: 3, 7, 14-15, 17 and 19-20.

 "Stringent conditions" as used herein refer to conditions such as those specified in US Patent No. 5,342,774, i.e., 18 hours of hybridization at 65°C, followed by four one-hour washes with 2x SSC, 0.1% SDS,
20 and a final wash with 0.2x SSC, more preferably 0.1x SSC, and 0.1% SDS for 30 minutes, as well as alternate conditions which afford the same level of stringency, and more stringent conditions.

 In accordance with the present invention,
25 molecules having a sequence, the complementary sequence of which hybridizes under stringent conditions to any one of SEQ ID NOS: 3, 7, 14-15, 17 and 19-20, can include nucleic acid molecules having substantial homology to any one of SEQ ID NOS: 3, 7, 14-15, 17 and
30 19-20; parts of SEQ ID NOS: 3, 7, 14-15, 17 and 19-20; degenerate sequences; and modified forms of SEQ ID NOS: 3, 7, 14-15, 17 and 19-20, such as mutant forms with base pair substitutions, deletions or insertions. In

the event that SEQ ID NOS: 3, 7, 14-15, 17 and 19-20 are fragments of full-length genes, such genes are also contemplated by the present invention as nucleic acid molecules having a sequence, the complementary sequence of which hybridizes under stringent conditions to any one of SEQ ID NOS: 3, 7, 14-15, 17 and 19-20.

As used herein, "a part" of a nucleic acid molecule refers to a fragment of the nucleic acid molecule having sufficient length to encode an antigenic peptide of at least 8 or 9 amino acids. In particular, the present invention contemplates "unique" fragments of nucleic acid molecules of SEQ ID NOS: 3, 7, 14-15, 17 and 19-20. A unique fragment is one that is a "signature" for the larger nucleic acid molecule. It is, for example, long enough to selectively distinguish the sequence of interest from others. As will be recognized by those skilled in the art, the size of the unique fragment will depend upon its conservancy in the genetic code. Thus, some regions of SEQ ID NOS: 3, 7, 14-15, 17 and 19-20 will require longer segments to be unique while others will require only shorter segments, typically between 12 and 32 nucleotides. Those skilled in the art are well versed in methods for selecting such sequences, e.g., by comparing the sequence of the fragment to those in known databases. *In vitro* confirmatory hybridization and sequencing analysis may also be used. According to the present invention, the unique fragments do not include sequences present in the prior art, such as ESTs and the like. Further according to the present invention, a unique fragment can be a functional fragment. A functional fragment of a nucleic acid molecule of the present invention is a fragment which

retains some functional property of the larger nucleic acid molecule, such as a fragment that encodes an antigenic epitope associated with melanoma or thyroid tumors.

5 The skilled artisan is fully capable of making, by following routine procedures, a nucleic acid molecule, the complement sequence of which hybridizes under stringent conditions to any one of SEQ ID NOS: 3, 7, 14-15, 17 and 19-20. The skilled artisan can
10 determine, for example, whether SEQ ID NOS: 3, 7, 14-15, 17 and 19-20 encompasses a complete open reading frame, and if not, can isolate the full length molecules that encompass a complete open reading frame by following standard procedures, e.g., DNA
15 hybridization-based cloning. See, e.g., Sambrook et al., 1989, *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory Press, New York.

20 The skilled artisan is also able to make fragments of these isolated nucleic acid molecules by using standard recombinant cloning techniques. The skilled artisan can further determine whether a fragment of an isolated nucleic acid molecule encodes the antigen(s) responsible for the immune response
25 elicited in the patient and the resulting hyper-immunoreactive serum. This can be accomplished by following a number of well-known methods. For example, various portions of a nucleic acid molecule can be cloned into an appropriate expression vector which can
30 be subsequently introduced into a desired host cell. Afterwards, polypeptides or peptides expressed from the respective DNA fragments can be tested for antigenicity by, e.g., using the patient's serum in a binding assay

5 routinely used in the SEREX methodology as described hereinabove; or using CTL clones with pre-defined specificity. Alternatively, one skilled in the art can chemically synthesize polypeptide or peptide fragments directly based on the nucleotide sequence of a fragment, and the antigenicity of the peptide can be determined by the reactivity toward the patient's serum in a binding assay, for example.

10 The skilled artisan is also able to isolate nucleic acid molecules having substantial homology to any one of SEQ ID NOS: 3, 7, 14-15, 17 and 19-20 by following standard procedures, e.g., DNA hybridization-based cloning procedure. See, e.g., Sambrook et al. (1989).

15 In another embodiment, the nucleic acid molecules of the present invention or parts thereof have been inserted into expression vectors. The choice of vectors can be determined by those skilled in the art. When the host cell is a eukaryotic cell, viral (e.g., retroviral, adenoviral or pox), yeast or
20 baculoviral vectors are preferred. When the host cell is a prokaryotic, then phage vectors are preferred, such as a λ phage vector. It is routine for those skilled in the art to construct expression vectors in
25 which a nucleic acid molecule of interest is placed in operable linkage to a desired promoter so as to effect the expression of the polypeptide or peptide encoded by such nucleic acid molecule in host cells. See, e.g., Sambrook et al. (1989).

30 The present invention also provides expression vectors which include nucleic acid molecules encoding a series of epitopes, known as "polytopes" (Thompson et al. (1995) in *Proc. Natl. Acad. Sci. USA*

92: 5845-5849; Gilbert et al., *Nature Biotechnol.* 15:
1280- 1284, 1997). The epitopes can be arranged in
sequential or overlapping fashion, with or without the
natural flanking sequences, and can be separated by
5 unrelated linker sequences if desired. The polytope is
processed in host cells to generate individual epitopes
which can be recognized by the immune system. Thus,
for example, peptides derived from the polypeptide
having an amino acid sequence encoded by any one of the
10 nucleic acid molecules of SEQ ID NOS: 3, 7, 14-15, 17
and 19-20 of the instant invention, which are presented
by MHC molecules and recognized by CTL or T helper
lymphocytes can be combined with peptides from other
tumor rejection antigens (e.g., by preparation of
15 hybrid nucleic acids or polypeptides) to form
"polytopes". Exemplary tumor associated peptide
antigens that can be administered to induce or enhance
an immune response are derived from tumor associated
genes and encoded proteins including MAGE-1, MAGE-2,
20 MAGE-3, MAGE-4, MAGE-5, MAGE-6, MAGE-7, MAGE-8, MAGE-9,
MAGE-10, MAGE-11, GAGE-1, GAGE-2, GAGE-3, GAGE-4, GAGE-
5, GAGE-6, BAGE-1, RAGE-1, LB33/MUM-1, DAGE, NAG, MAGE-
Xp2, MAGE-Xp3, MAGE-Xp4, tyrosinase, brain glycogen
phosphorylase, Melan-A, and MAGE-C1. For example,
25 antigenic peptides characteristic of tumors include
those listed in Table I below.

30

Table I: Exemplary Antigens

| Gene | MHC | Peptide | Position | SEQ ID NO: |
|---------------------------|----------|---------------------------|-------------------|------------|
| MAGE-1 | HLA-A1 | EADPTGHSY | 161-169 | 21 |
| | HLA-Cw16 | SAYGEPRKL | 230-238 | 22 |
| MAGE-3 | HLA-A1 | EVDPIGHLY | 168-176 | 23 |
| | HLA-A2 | FLWGPRLV | 271-279 | 24 |
| | HLA-B44 | MEVDPIGHLY | 167-176 | 25 |
| BAGE | HLA-Cw16 | AARAVFLAL | 2-10 | 26 |
| GAGE-1,2 | HLA-Cw16 | YRPRPRRY | 9-16 | 27 |
| RAGE | HLA-B7 | SPSSNRIRNT | 11-20 | 28 |
| GnT-V | HLA-A2 | VLPDVFIRC(V) | 2-10/11 | 29 |
| MUM-1 | HLA-B44 | EEKLIVVLF | exon 2/ intron | 30 |
| | | EEKLSVVLF (wild type) | | 31 |
| CDK4 | HLA-A2 | ACDPHSGHFV | 23-32 | 32 |
| | | ARDPHSGHFV (wild type) | | 33 |
| β -catenin | HLA-A24 | SYLDSGIHF | 29-37 | 34 |
| | | SYLDSGIHS (wild type) | | 35 |
| Tyrosinase | HLA-A2 | MLLAVLYCL | 1-9 | 36 |
| | HLA-A2 | YMNGTMSQV | 369-377 | 37 |
| | HLA-A2 | YMDGTMSQV | 369-377 | 38 |
| | HLA-A24 | AFLPWHRLF | 206-214 | 39 |
| | HLA-B44 | SEIWRDIDF | 192-200 | 40 |
| | HLA-B44 | YEIWRDIDF | 192-200 | 41 |
| | HLA-DR4 | QNILLSNAPLGP QFP | 56-70 | 42 |
| | HLA-DR4 | DYSYLQSDPDPS FQD | 448-462 | 43 |
| Melan-A ^{MART-1} | HLA-A2 | (E)AAGIGILTV | 26/27-35 | 44 |
| | HLA-A2 | ILTVILGVL | 32-40 | 45 |
| gp100 ^{Pmel17} | HLA-A2 | KTWGQYWQV | 154-162 | 46 |
| | HLA-A2 | ITDQVPFSV | 209-217 | 47 |
| | HLA-A2 | YLEPGPVTA | 280-288 | 48 |
| | HLA-A2 | LLDGTATLRL | 457-466 | 49 |
| | HLA-A2 | VLYRYGSFSV | 476-485 | 50 |
| DAGE | HLA-A24 | LYVDSLFFL | 301-309 | 51 |
| MAGE-6 | HLA-Cw16 | KISGGPRISYPL | 292-303 | 52 |

The peptides of SEQ ID NOS: 41, 51 and 52 are presented in U.S. Application Serial No. 08/724,774, PCT Application Publication No. W096/10577 and U.S. Application Serial No. 08/713,354, respectively. Other exemplary peptides include those listed in U.S. Patent

Applications 08/672,351, 08/669,590, 08/487,135,
08/530,569 and 08/880,693. Other examples are known to
one of ordinary skill in the art (for example, see
Coulie, *Stem Cells* 13: 393-403, 1995), and can be used
5 in the invention in a like manner as those disclosed
herein.

It is known that tumors express a set of
tumor antigens, of which only certain subsets may be
expressed in the tumor of any given patient. Polytopes
10 can be prepared which correspond to the different
combination of epitopes representing the subset of
tumor rejection antigens expressed in a particular
patient. Polytopes also can be prepared to reflect a
broader spectrum of tumor rejection antigens known to
15 be expressed by a tumor type.

The present invention further contemplates
host cells for propagating and/or expressing the
nucleic acid molecules of the present invention. Those
skilled in the art are equally familiar with the choice
20 of cell lines and the procedures to transform or
transfect such cell lines. Examples of the cell lines
include, but are not limited to, eukaryotic cells such
as COS cells (e.g., COS-7), CHO cells (e.g., CHO-1),
NIH 3T3 cells, yeast cells (e.g., strains of
25 *Saccharomyces* or *Pichia pastoris*), insect cells (e.g.,
Spodoptera frugiperda); and prokaryotic cells such as
strains of *E. coli*, strains of *Pseudomonas* (e.g.,
Pseudomonas aeruginosa) or strains of *Bacillus*.

In a preferred embodiment, the present
30 invention provides an antigen presenting cell
transformed with an expression vector as described
hereinabove.

"Antigen presenting cells" as used herein refer to cells expressing at least one MHC class I or class II molecule, which include, but are not limited to, professional antigen presenting cells such as B cells, monocytes, macrophages, dendritic cells and T cells; and facultative antigen presenting cells such as fibroblasts and endothelium cells. Antigen presenting cells can be isolated from tissue or blood samples. Both normal and malignant cells can be employed. Cell lines established in tissue culture from such samples can also be used. Many such cell lines are available from American Type Culture Collection (ATCC), Rockville, Maryland. Those skilled in the art can determine whether a chosen antigen presenting cell expresses at least one MHC molecule that is capable of presenting a peptide derived from a particular nucleic acid molecule. See, e.g., Coligan et al. (1994). Such cell can then be transfected with an expression vector which, under appropriate conditions, leads to the expression on the cell surface of one or more antigenic peptides encoded by fragments of the nucleic acid molecule of interest, complexed with appropriate MHC molecules,.

Another embodiment of the present invention is directed to proteins encoded by the isolated nucleic acid molecules of SEQ ID NOS: 3, 7, 14-15, 17 and 19-20 or parts thereof.

The term "protein" used herein refers to both the unmodified forms (precursors) and post-translationally modified forms of a protein. Eukaryotic cells are well known for their ability to post-translationally modify proteins, so as to produce glycoproteins and lipoproteins, for example. According

to the present invention, the term "protein" also encompasses polypeptides and peptides.

5 The term "polypeptide" as used herein refers to a chain of at least 10 contiguous amino acids. The term "peptide" used herein refers to a chain of at least 8 or 9 amino acids.

10 The protein encoded by a nucleic acid molecule can be produced by routine recombinant expression in a desired host cell and subsequently purified by various known procedures, such as chromatography. A polypeptide or peptide can also be chemically synthesized according to its coding sequence in a standard peptide synthesizer. Those skilled in the art can also isolate antigenic peptides directly from the MHC/peptide complexes of antigen-expressing cells by, e.g., a method disclosed by Mandelblom et al. (1994). According to such method, peptides are eluted from the MHC-peptide complexes at the surface of antigen-expressing cells. The resulting pools of peptides are fractionated by HPLC and screened with antigen-specific CTL clones. Specific antigenic peptides can be identified and isolated based upon their ability to provoke specific CTL clones.

25 Purified proteins can be used as immunogens, either alone or in combination with an adjuvant such as saponins, GM-CSF, or interleukins. Immunogens such as these may be used, for example, to generate antibodies.

30 Accordingly, the present invention also contemplates antibodies directed against the proteins encoded by the nucleic acid molecules of SEQ ID NOS: 3, 7, 14-15, 17 and 19-20 or parts thereof.

There are a variety of ways to obtain specific antibodies. Antibodies can be generated by

administering a protein of interest, either alone or in combination with an adjuvant, to various hosts, such as a rabbit, a mouse, or a sheep. Both monoclonal or polyclonal antibodies can be obtained using such immunized host. The methods for generating polyclonal and monoclonal antibodies are well known in the art. See, e.g., Coligan et al. *Current Protocols in Immunology*, John Wiley & Sons Inc., New York, New York (1994). Fragments of antibodies, such as Fab, F(ab)₂, and the like, as well as recombinantly produced antibodies, are also contemplated by the present invention.

Another embodiment of the present invention is directed to isolated peptide/HLA complexes. Preferably, the peptide in such isolated peptide/HLA complexes is encoded by a fragment of any one of SEQ ID NOS: 3, 7, 14-15, 17 and 19-20.

According to this embodiment, once the type of the HLA molecule capable of presenting a peptide is ascertained, such HLA molecule can be produced by any appropriate recombinant expression system, e.g., an *E. coli*-based expression system. As described above, peptides can be obtained by a number of ways, such as chemical synthesis or recombinant expression. The peptides and the presenting HLA molecules can then be mixed *in vitro* under conditions that favor the formation of HLA/peptide complexes. Such conditions are well known in the art. See, e.g., Garboczi et al. (*Proc. Natl. Acad. Sci. USA* 89: 3429-3433, 1992 and Altman et al. (*Science* 274: 94-96, 1996).

In another embodiment, the present invention provides methods of diagnosing a pathological condition

characterized by an abnormal expression of one or more of the nucleic acid molecules of the present invention.

The term "diagnosing" as used herein encompasses determining or monitoring the onset of, the progression of, the regression of, or the efficacy of a therapeutic regime for, a pathological condition.

Pathological conditions characterized by an abnormal expression of one or more of the nucleic acid molecules SEQ ID NOS: 1-30 of the present invention include, but are not limited to melanoma, the presence of a thyroid tumor, rectal cancer, lung cancer, breast cancer and colon cancer.

Diagnosis of a pathological condition can be accomplished by determining an abnormal expression of at least one, i.e., one or more, nucleic acid molecule that is associated with such pathological condition. By comparing the expression in a sample from a patient suffering a pathological condition, with the expression in a normal sample, the skilled artisan can readily determine whether a relevant nucleic acid molecule is abnormally expressed in such pathological condition.

The abnormal expression of a nucleic acid molecule can manifest as an abnormal level of the mRNA of such nucleic acid molecule, the protein or peptide fragments encoded by such nucleic acid molecule, serum antibodies against such protein or peptide fragments, peptide/MHC complexes at the cell surface, or CTLs specific for certain peptide/MHC complexes. Accordingly, there are various assays which can be employed to detect the abnormal expression of a subject nucleic acid molecule.

A sample of suspected abnormality can be taken from a patient, such as a tissue biopsy sample,

or body fluid sample such as serum. The expression of a protein of interest in such sample can be determined by a variety of diagnostic assays.

One type of diagnostic assay is based on
5 determination of the level of mRNA of a nucleic acid molecule associated with the pathological condition in question. Thus, for example, diagnosis of melanoma can be based on assaying the level of mRNA of, preferably, the repressor protein-encoding gene (SEQ ID NO: 21),
10 the KIAA0201 gene (SEQ ID NO: 22), the Ki-67-encoding gene (SEQ ID NOS: 23 and 24), the CENP-B-encoding gene (SEQ ID NO: 25), or nucleic acid sequences encompassing SEQ ID NO: 3 or 7. Diagnosis of thyroid tumors can be based on assaying the level of mRNA of, preferably, the
15 TAFII68-encoding gene (SEQ ID NO: 26), lipocortin II-encoding gene (SEQ ID NO: 27), the thyroglobulin-encoding gene (SEQ ID NO: 28), the thymosin-encoding gene (SEQ ID NO: 29), the acid ceramidase-encoding gene (SEQ ID NO: 30), or nucleic acid sequences encompassing
20 one of SEQ ID NOS: 14-15, 17 and 19-20. Similarly, diagnosis of rectal, lung, breast, colon cancer or any other pathological condition can be based on assaying the level of the mRNA of one or more of SEQ ID NOS: 3, 7, 14-15, 17, 19-30 that are associated with the
25 relevant pathological condition. For example, diagnosis of rectal cancer can be based on determining the level of preferably, the mRNA of one or more of SEQ ID NOS: 21-24, 26, or 30, or the mRNA of a nucleic acid molecule encompassing any one of SEQ ID NOS: 14-15 or
30 20. Diagnosis of lung cancer can be based on determining the level of preferably, the mRNA of one or more of SEQ ID NOS: 21 and 23-25, or the mRNA of a nucleic acid molecule encompassing any one of SEQ ID

NOS: 14-15 or 20. Diagnosis of breast cancer can be based on determining the level of, preferably, the mRNA of any one of SEQ ID NOS: 23 or 24, or the mRNA of a nucleic acid molecule encompassing SEQ ID NOS: 15.

5 Diagnosis of colon cancer can be based on determining the level of preferably, the mRNA of one or more of SEQ ID NOS: 21-24, 26 or 29-30, or the mRNA of a nucleic acid molecule encompassing any one of SEQ ID NOS: 14-15 or 19-20. The methods for determining the level of
10 mRNA are well within the ken of those skilled in the art, such as Northern Blot analysis or PCR analysis.

Another type of diagnostic assay is based on determination of the amount of protein expressed from the nucleic acid molecules associated with the
15 pathological condition in question, or parts of such proteins. For example, for diagnosing melanoma, the protein to be examined can be the repressor protein encoded by SEQ ID NO: 21, the protein encoded by KIAA0201 (SEQ ID NO: 22), Ki-67 antigen (encoded by SEQ
20 ID NO: 23 or 24), CENP-B (encoded by SEQ ID NO: 25) or the protein encoded by any one of the nucleic acid sequences encompassing SEQ ID NO: 3, or 7. Preferably, diagnosis of melanoma is based on detecting proteins encoded by any one of SEQ ID NOS: 1-10. For diagnosing
25 thyroid tumors, the protein to be examined can be TAFII68 (encoded by SEQ ID NO: 26), lipocortin II (encoded by SEQ ID NO: 27), thyroglobulin (encoded by SEQ ID NO: 28), thymosin (encoded by SEQ ID NO: 29), the acid ceramidase (encoded by SEQ ID NO: 30), or a
30 protein encoded by any one of the nucleic acid sequences encompassing one of SEQ ID NOS: 14-15, 17 and 19-20. Preferably, diagnosis of the presence of a thyroid tumor is based on detecting proteins encoded by

any one of SEQ ID NOS: 11-20. Similarly, diagnosis of rectal, lung, breast or colon cancer, or any other pathological condition can be based on assaying one or more proteins encoded by any one, i.e., one or more, of SEQ ID NOS: 1-30, that is associated with the relevant cancer. One skilled in the art can use various assays including, e.g., SDS-gels or 2D gels, Western Blot Analysis, ELISA and immunofluorescence flow-cytometry.

Still another type of diagnostic assay is based on detection of antibodies in the serum that are specific for a protein associated with a pathological condition in question or parts of such protein. Thus, in this type of assay, antibodies are detected by using the specific antigens in assays such as Western Blot or affinity chromatography, or a SEREX screening assay described herein. Antibodies specific for an antigenic peptide can also be detected by using cells which express and present the antigenic peptide at the surface in the context of an MHC molecule via assays such as FACS.

Another type of diagnostic assay is based on detection of cells in the patient's sample, which cells have at their surface, a peptide encoded by a fragment of a nucleic acid molecule associated with the pathological condition in question. For example, for diagnosing melanoma, such nucleic acid molecule includes the gene encoding the repressor protein (SEQ ID NO: 21), the KIAA0201 gene (SEQ ID NO: 22), the Ki-67 encoding gene (SEQ ID NO: 23 and 24), the CENP-B-encoding gene (SEQ ID NO: 25), or the nucleic acid sequences encompassing SEQ ID NO: 3, or 7; and preferably, such nucleic acid molecule is any one of SEQ ID NOS: 1-10. For diagnosing thyroid tumors, such

nucleic acid molecule includes genes encoding TAFII68 (SEQ ID NO: 26), lipocortin II (SEQ ID NO: 27), thyroglobulin (SEQ ID NO: 28), thymosin (SEQ ID NO: 29), or the acid ceramidase-encoding gene (SEQ ID NO: 30), or any one of the nucleic acid sequences encompassing one of SEQ ID NOS: 14-15, 17 and 19-20; and preferably, such nucleic acid molecule is any one of SEQ ID NOS: 11-20. Likewise, for diagnosing rectal, lung, breast or colon cancer, the nucleic acid molecule can include any one of SEQ ID Nos: 1-30 that is associated with the relevant cancer. To determine the presence of such cell in a patient's sample, cellular-immuno assays can be employed, e.g., FACS analysis using antibodies raised against such peptide, or cytotoxic assays using pre-established CTLs specific for such peptide.

Another type of diagnostic assay is based on detection of CTLs in the patient's sample that are specific for a peptide of a protein associated with the pathological condition in question. Methods for detecting CTLs specific for an antigen are known in the art and are described hereinabove, such as assays for ⁵¹Cr release, TNF production or IFN-gamma production.

According to the present invention, the present methods of diagnosis are applicable not only to the pathological conditions exemplified, such as melanoma, the presence of a thyroid tumor, rectal cancer, lung cancer, breast cancer or colon cancer, but also to pathological conditions in general that are characterized by an abnormal expression of one or more of the subject nucleic acid molecules of the present invention. The isolated nucleic acid molecules of the present invention are clearly expressed in an abnormal

manner in patients having melanoma, thyroid tumor, rectal, lung, breast or colon cancer. These molecules may also be expressed abnormally in other tumors or in cells associated with other pathological disorders.

5 Thus, the techniques described hereinabove can be employed for diagnosing a pathological condition characterized by an abnormal expression of one of the nucleic acid molecules having a sequence encompassing one or more of SEQ ID NOS: 1-20.

10 In another embodiment, the present invention provides pharmaceutical compositions. The pharmaceutical compositions of the present invention are useful for treating pathological conditions characterized by an abnormal expression of one or more
15 of the instant nucleic acid molecules of the present invention.

One pharmaceutical composition of the present invention includes an antisense molecule of one of the repressor protein-encoding gene (SEQ ID NO: 21), the
20 KIAA0201 gene (SEQ ID NO: 22), the Ki-67 encoding gene (SEQ ID NO: 23 and 24), the CENP-B encoding gene (SEQ ID NO: 25), nucleic acid sequences encompassing SEQ ID NO: 3, or 7, the TAFII68-encoding gene (SEQ ID NO: 26), lipocortin II-encoding gene (SEQ ID NO: 27), the
25 thyroglobulin -encoding gene (SEQ ID NO: 28), the thymosin-encoding gene (SEQ ID NO: 29), the acid ceramidase-encoding gene (SEQ ID NO: 30), and nucleic acid sequences encompassing one of SEQ ID NOS: 14-15, 17 and 19-20, or parts of such nucleic acid molecules.
30 Preferably the antisense molecule is about 10-100 nucleotides in length and is carried by a suitable vector, such as a retroviral vector or a viral vector. The choice of vectors for such purpose is well-known in

the art, e.g., Vaccinia. The use of antisense molecules for inhibiting gene expression is known in the art.

5 Another pharmaceutical composition of the present invention includes a protein encoded by one of the repressor protein-encoding gene (SEQ ID NO: 21), the KIAA0201 gene (SEQ ID NO: 22), the Ki-67 encoding gene (SEQ ID NO: 23 and 24), the CENP-B encoding gene (SEQ ID NO: 25), nucleic acid sequences encompassing
10 SEQ ID NO: 3, or 7, the TAFII68-encoding gene (SEQ ID NO: 26), lipocortin II-encoding gene (SEQ ID NO: 27), the thyroglobulin-encoding gene (SEQ ID NO: 28), the thymosin-encoding gene (SEQ ID NO: 29), the acid ceramidase-encoding gene (SEQ ID NO: 30), nucleic acid
15 sequences encompassing one of SEQ ID NOS: 14-15, 17 and 19-20, or parts of such nucleic acid molecules. Preferably, the protein is encoded by one of SEQ ID NOS: 1-20 or parts thereof. Such proteins can be administered to a subject to provoke or augment an
20 immune response in the subject against the abnormally expressed proteins.

Still another pharmaceutical composition of the present invention includes an antibody specific for a protein encoded by one of the repressor protein-
25 encoding gene (SEQ ID NO: 21), the KIAA0201 gene (SEQ ID NO: 22), the Ki-67 encoding gene (SEQ ID NO: 23 and 24), the CENP-B encoding gene (SEQ ID NO: 25) and nucleic acid sequences encompassing SEQ ID NO: 3, or 7, the TAF 1168-encoding gene (SEQ ID NO: 26), lipocortin
30 II-encoding gene (SEQ ID NO: 27), the thyroglobulin-encoding gene (SEQ ID NO: 28), the thymosin-encoding gene (SEQ ID NO: 29), the acid ceramidase-encoding gene (SEQ ID NO: 30), and nucleic acid sequences

encompassing one of SEQ ID NOS: 14-15, 17 and 19-20, or parts of these nucleic acid molecules. Preferably, the antibody is specific for a protein encoded by any one of SEQ ID NOS: 1-20 or parts of such proteins. Both
5 polyclonal antibodies and monoclonal antibodies can be used. Monoclonal antibodies are preferred.

Another pharmaceutical composition of the present invention includes an antigen-presenting cell having at the cell surface, in the context of MHC
10 molecules, one or more antigenic peptides encoded by a fragment(s) of one of the repressor protein-encoding gene (SEQ ID NO: 21), the KIAA0201 gene (SEQ ID NO: 22), the Ki-67 encoding gene (SEQ ID NO: 23 and 24), the CENP-B encoding gene (SEQ ID NO: 25) and nucleic
15 acid sequences encompassing SEQ ID NO: 3, or 7, the TAFII68-encoding gene (SEQ ID NO: 26), lipocortin II - encoding gene (SEQ ID NO: 27), the thyroglobulin- encoding gene (SEQ ID NO: 28), the thymosin-encoding gene (SEQ ID NO: 29), the acid ceramidase-encoding gene
20 (SEQ ID NO: 30), nucleic acid sequences encompassing one of SEQ ID NOS: 14-15, 17 and 19-20. The antigen presenting cells to be used in the pharmaceutical composition of the present invention express MHC molecules that are compatible with the MHC molecules of
25 the patient being treated. At least one of the MHC molecules expressed by such cells is capable of presenting a peptide encoded by a fragment of a subject nucleic acid molecule. The choice of antigen presenting cells is described hereinabove.

30 In accordance with the present invention, antigen presenting cells can be further modified to express other molecules for augmenting immunogenicity. A number of immune response potentiating molecules can

be used, including lymphokines, costimulatory molecules such as B7-1 (CD80), B7-2 (CD86), LFA-3, LFA-1 and CD40. B7 molecules, by interacting with CD28 or CTLA-4 molecules on T cells, potentiate T cell proliferation and effector function such as antitumor activity. See, e.g., Zheng et al., *Proc. Natl. Acad. Sci. USA* 95: 6284-6289 (1998); Wang et al., *J. Immunol.* 19: 1-8 (1996). The interaction of LFA-3 on antigen presenting cells with CD2 on T cells induces T cell to produce IL-2 and IFN-gamma (Fenton et al., *J. Immunol.* 21(2): 95-108, 1998). Complete CTL activation and effector function requires Th cell help through the interaction between the CD40 ligand expressed on Th cells and the CD40 molecules expressed on antigen presenting cells (Ridge et al., *Nature* 393:474, 1998; Bennett et al., *Nature* 393: 478, 1998; and Achenberger et al., *Nature* 393: 480, 1998). These additional immune-potentiating molecules can be included in any of the expression vectors (such as retroviral, adenoviral, or pox vectors) and introduced into antigen presenting cells by, e.g., transfection.

The pharmaceutical compositions of the present invention can also include a pharmaceutical acceptable carrier. As used herein, a pharmaceutically acceptable carrier includes any and all solvents, including water, dispersion media, culture from cell media, isotonic agents and the like that are non-toxic to the patient. Preferably, it is an aqueous isotonic buffered solution with a pH of around 7.0. The use of such media and agents in therapeutic compositions is well known in the art. Except insofar as any conventional media or agent is incompatible with the pharmaceutical compositions of the present invention,

use of such conventional media or agents in the pharmaceutical compositions are contemplated. Supplementary active ingredients can also be incorporated into the compositions.

5 In a further embodiment, the pharmaceutical compositions of the present invention are used to treat pathological conditions characterized by an abnormal expression of one or more of the instant nucleic acid molecules of the present invention. Accordingly, the
10 present invention provides methods of treating a subject suffering a pathological condition characterized by an abnormal expression of one or more of the instant nucleic acid molecules, by administering to such subject a therapeutically effective amount of a
15 pharmaceutical composition of the present invention.

 The term "treating" means delaying the onset of a pathological condition or alleviating a pathological condition by controlling the expression of the nucleic acid molecule being abnormally expressed
20 under such pathological condition. "Alleviating" is indicated by, in the case of tumor, inhibition of tumor growth, reduction in tumor size, inhibition of tumor metastasis and the like.

 "A pathological condition" as defined
25 hereinabove, includes, but is not limited to, melanoma the presence of a thyroid tumor, rectal cancer, lung cancer, breast cancer or colon cancer. For treating melanoma, pharmaceutical compositions derived from melanoma-associated nucleic acid molecules (such as
30 antisense molecules, proteins, antibodies or cells) are preferred. For treating thyroid tumors, pharmaceutical compositions derived from thyroid tumor-associated nucleic acid molecules are preferred. Likewise, for

treating any other pathological condition, such as rectal cancer, lung cancer, breast cancer or colon cancer, preferred pharmaceutical compositions to be used in the treatment are those derived from the nucleic acid molecules associated with that condition.

One method of treating a subject having a pathological condition characterized by an abnormal expression of a nucleic acid molecule of the present invention is by administering to the subject, an antisense molecule of such nucleic acid molecule or parts thereof. For example, a subject having melanoma can be treated by administering to the subject, one or more of an antisense molecule of the repressor protein-encoding gene (SEQ ID NO: 21), the KIAA0201 gene (SEQ ID NO: 22), the Ki-67 encoding gene (SEQ ID NO: 23 and 24), the CENP-B encoding gene (SEQ ID NO: 25), or nucleic acid sequences encompassing SEQ ID NO: 3, or 7, or parts of these nucleic acid molecules; a subject having thyroid tumors can be treated by administering to the subject one or more of an antisense molecule of the TAFII68-encoding gene (SEQ ID NO: 26), lipocortin II-encoding gene (SEQ ID NO: 27), the thyroglobulin-encoding gene (SEQ ID NO: 28), the thymosin-encoding gene (SEQ ID NO: 29), the acid ceramidase-encoding gene (SEQ ID NO: 30), and nucleic acid sequences encompassing one of SEQ ID NOS: 14-15, 17 and 19-20, or parts of these nucleic acid molecules.

Preferably, the antisense molecule is contained in a vector suitable for expression in the subject being treated. The choice of vectors for such purpose is well-known in the art and can be viral or retroviral vectors, e.g., a Vaccinia vector. A vector carrying the antisense DNA can be administered to a

subject in an amount sufficient to inhibit the expression of the protein. Such vector can be administered alone or with a carrier, such as a liposome, which facilitates the incorporation of the vector into a cell.

Another method of treating a subject having a pathological condition characterized by an abnormal expression of a nucleic acid molecule of the present invention is by administering to the subject, a protein encoded by such nucleic acid molecule or parts thereof. For example, a subject having melanoma can be treated by administering to the subject, the repressor protein (encoded by SEQ ID NO: 21), the protein encoded by KIAA0201 (SEQ ID NO: 22), Ki-67 (encoded by SEQ ID NO: 23 or 24), CENP-B (encoded by SEQ ID NO: 25), a protein encoded by any one of the nucleic acid sequences encompassing SEQ ID NO: 3, or 7, or parts or combinations thereof. A subject having thyroid tumors can be treated by administering to the subject, TAF II68 (encoded by SEQ ID NO: 26), lipocortin II (encoded by SEQ ID NO: 27), thyroglobulin (encoded by SEQ ID NO: 28), thymosin (encoded by SEQ ID NO: 29), the acid ceradimase encoded by SEQ ID NO: 30), a protein encoded by any one of the nucleic acid sequences encompassing one of SEQ ID NOS: 14-15, 17 and 19-20, or parts or combinations thereof.

The proteins are administered in an amount sufficient to provoke or augment an immune response in the subject which eliminate the abnormally expressed proteins. The proteins can be combined with one or more of the known immune adjuvants, such as saponins, GM-CSF, interleukins and so forth. Small peptides may

also be coupled to the well-known conjugates to achieve the desired immunogenicity.

5 Still another method of treating a subject having a pathological condition characterized by an abnormal expression of a nucleic acid molecule of the present invention is by administering to the subject, an antibody directed against the protein encoded by such nucleic acid molecule or parts thereof. For example, a subject having melanoma can be treated by
10 administering to the subject, one or more of an antibody directed against the repressor protein (encoded by SEQ ID NO: 21), the protein encoded by the KIAA0201 (SEQ ID NO: 22), Ki-67 (encoded by SEQ ID NO: 23 or 24), CENP-B (encoded by SEQ ID NO: 25), or a
15 protein encoded by any one of the nucleic acid sequences encompassing SEQ ID NO: 3, or 7, or parts of these proteins. A subject having thyroid tumors can be treated by administering to the subject, one or more of an antibody directed against TAFII68 (encoded by SEQ ID
20 NO: 26), lipocortin II (encoded by SEQ ID NO: 27), thyroglobulin (encoded by SEQ ID NO: 28), thymosin (encoded by SEQ ID NO: 29), the acid ceramidase (encoded by SEQ ID NO: 30), or a protein encoded by any one of the nucleic acid sequences encompassing one of
25 SEQ ID NOS: 14-15, 17 and 19-20, or parts of these proteins. The antibodies can be administered alone or with pharmaceutically acceptable carriers in an amount sufficient to inhibit the function of the protein or proteins.

30 Still another method of treating a subject having a pathological condition characterized by an abnormal expression of a nucleic acid molecule of the present invention is by administering to the subject,

an antigen presenting cell having one or more antigenic peptides complexed with MHC molecules, which peptides are encoded by fragments of such nucleic acid molecule.

5 The cells are preferably treated to be rendered non-proliferative before the administration to the subject suffering a relevant pathological condition. The cells are administered to a patient in an amount sufficient to stimulate an immune response against the protein that is abnormally expressed in the patient. Such cells may present epitopes to T cells and/or B cells, leading to a cellular immune response and/or a humoral immune response in the subject. According to the present invention, the induced immune response can alleviate the pathological condition by
10 cytotoxic killing and/or antibody-mediated killing of the cells of abnormality.
15

In addition to direct administration to a subject for treatment, antigen presenting cells expressing an MHC/peptide complex of interest can be used in an *ex vivo* regime to generate cytolytic T cells specific for the peptide being presented. The
20 procedure to develop such specific CTLs *in vitro* is known in the art, e.g., as disclosed by the United States Patent No. 5,342,774. Briefly, a blood sample containing T cell precursors is taken from a subject, preferably, the autologous patient. PBLs are purified from such blood sample and are incubated with stimulator cells, in this case, the antigen presenting cells expressing a MHC/peptide complex. Specific CTLs
25 are thus produced which can be detected by standard assays, such as Cr^{51} release or secretion of IFN-gamma. CTL cells generated as such can be reperfused to the patient and alleviate the pathological condition by
30

lysing the cells abnormally expressing the peptide/MHC complex. See related teachings by Greenberg (1986) *J. Immunol.* 136 (5): 1917; Riddel et al. (1992) *Science* 257: 238; Lynch et al. (1991) *Eur. J. Immunol.* 21: 1403; and Kast et al. (1989) *Cell* 59: 603.

For practicing the treatment methods of the present invention, a pharmaceutical composition as described hereinabove can be administered to a patient in need thereof in any convenient manner, e.g., by subcutaneous (s.c.), intraperitoneal (i.p.), intra-arterial (i.a.), or intravenous (i.v.) injection..

The precise amount of a pharmaceutical composition to be administered so as to be therapeutically effective, can be determined those skilled in the art with consideration of individual differences in age, weight, tumor size, severity of the pathological condition and so forth.

All the publications mentioned in the present disclosure are incorporated herein by reference. The terms and expressions which have been employed in the present disclosure are used as terms of description and not of limitation, and there is no intention in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, it being recognized that various modifications are possible within the scope of the invention.

The present invention is further illustrated but not limited by the following examples.

Example 1

Isolation of cDNA clones using the SEREX methodology.

Two thyroid tumor cDNA libraries and one
5 melanoma cDNA library were prepared, using standard
techniques. See Sambrook et al., 1989, *Molecular
Cloning: A Laboratory Manual*, Second Edition, Cold
Spring Harbor Laboratory Press, New York. The
libraries were screened using the SEREX methodology as
10 described supra and set forth by Sahin et al. (1995)
and by Chen et al., *Proc. Natl. Acad. Sci. USA* 94:
1914 (1997), incorporated herein by reference.

More specifically, total RNA was isolated
from tumor cells secured from three individuals,
15 Patient 1 with melanoma, Patients 2 and 3 with thyroid
tumors. The RNA from each patient was used to prepare
a cDNA library, resulting in three cDNA libraries,
named as Mel-N1, Thy-N1, and Thy-N2, respectively.
Each of these cDNA libraries was cloned into λ ZAP phage
20 vectors (Short et al., *Nucleic Acids Res.* 16: 7583,
1988). Bacteria of the strain *E. Coli* XL1-Blue was
then transfected with the recombinant phages derived
from one of the described phage cDNA libraries, plated
at a density of $4-5 \times 10^3$ pfus (plaque forming units)
25 per plate, and incubated for eight hours at 37°C. A
nitrocellulose membrane was then placed on each plate,
followed by overnight incubation.

The membrane was subsequently washed four
times with TBS containing 0.05% Tween-20, and was
30 immersed afterwards in TBS containing 5% non-fat dried
milk. After one hour, the nitrocellulose membranes
were washed three times with TBS, followed by the
incubation with diluted human serum secured from the

autologous patient. The serum was pretreated, as described in detail by Sahin et al. (1995), U.S. Patent No. 5,698,396 and International Application WO 96/40209, to deplete interfering antibodies directed against antigens derived from *E. Coli* and phages. The stripped human serum was diluted 1:100 in TBS containing 0.5% milk powder (w/v). The membranes were incubated in the human serum overnight with gentle shaking, followed by three washes with TBS. Afterwards, the membranes were incubated with polyclonal goat anti-human IgG Fcy conjugated with HRP. The conjugated antibodies were diluted 1:2000 in TBS-1% BSA. After incubation for one hour at room temperature, the membranes were washed three times with TBS. The positive clones were visualized using 30% solution of hydrogen peroxidase. Positive clones were further subcloned to monoclonality by repeated rounds of transfection and testing.

At the end of this screening procedure, ten cDNA clones (MEL 1-10) were obtained from the MEL-N1 library; three cDNA clones (Thy 1-3) were obtained from the Thy-N1 library; seven cDNA clones (Thy 5-6, 9, 11-12 and 14-15) were obtained from the Thy-N2 library.

Example 2

Sequencing the isolated cDNA clones.

5 The insert size of the isolated cDNA clones
was determined using restriction enzymes and listed in
Table I. The inserts of the cDNA clones were sequenced
from the 3' end using standard techniques. See
Sambrook et al. (1989), for example. SEQ ID NOS: 1-20
10 illustrate the sequences of the 3' portions of these
isolated cDNA clones. Following nucleotide homology
search of the databases, these sequences were resolved
into known and unknown sequences. Table 1 summarizes
the results. In Table 1, the "+" signs are used to
15 indicate the relative strength of reactivity of each
clone toward the corresponding patient serum.

SEQ ID NO: 1 (MEL 1) corresponds to a portion
of the partial mRNA sequence for the repressor protein
(SEQ ID NO: 21). SEQ ID NO: 2 (MEL 2) corresponds to a
portion of the KIAA0201 gene (SEQ ID NO: 22, homologue
20 to heat shock protein HSP). SEQ ID NOS: 4 and 8-10
(MEL 4 and MEL 8-10) correspond to portions of the Ki-
67 nuclear antigen gene (SEQ ID NO: 23 and 24). SEQ ID
NOS: 5-6 (Mel 5-6) correspond to portions of the CENP-B
gene (SEQ ID NO: 25). SEQ ID NO: 3 (MEL 3) is matched
25 by several EST sequences in Genbank. SEQ ID NO: 7 (MEL
7) does not find any sequence match in the databases.

SEQ ID NO: 11 (Thy 1) corresponds to a
portion of the TAFII68 (TBP associated factor) gene
(SEQ ID NO: 26). SEQ ID NO: 12 (Thy 2) corresponds to
30 a portion of the lipocortin II gene (SEQ ID NO: 27).
SEQ ID NO: 13 (Thy 3) corresponds to a portion of the
thyroglobulin gene (SEQ ID NO: 28). SEQ ID NO: 16 (Thy
9) corresponds to a portion of the thymosin beta-4 gene

(SEQ ID NO: 29). SEQ ID NO: 17 (Thy 12) corresponds to a portion of the Acid ceramidase gene (SEQ ID NO: 30). SEQ ID NOS: 14,17 and 19-20 (Thy 5, Thy 11, Thy 14 and Thy 15) are only matched by EST sequences in the

5 databases.

Table II

| SEQ ID NO | Clone | Serum react | Insert size (kb) | Access. No. | Identity |
|-----------|--------|-------------|------------------|-------------|---|
| 1 | Mel 1 | ++ | 0.4 | D30612 | mRNA (partial) for repressor protein |
| 2 | Mel 2 | +++++ | 0.7 | D86956 | KIAA0201, homolog to HSP |
| 3 | Mel 3 | + | 1.65 | Novel | EST matches |
| 4 | Mel 4 | ++++ | 0.9 | X65551/50 | Ki-67 nuclear antigen, LONY-BR-8 (Breast SEREX) |
| 8 | Mel 8 | +++ | 0.8 | | |
| 9 | Mel 9 | ++++ | 0.9 | | |
| 10 | Mel 10 | ++++ | 1.0 | | |
| 5 | Mel 5 | ++ | 1.25 | X55039 | CENP-B centromere autoantigen |
| 6 | Mel 6 | +++ | 1.2 | | |
| 7 | Mel 7 | +++ | 0.9 | Novel | No EST match |
| 11 | Thy 1 | + | 0.8 | X98893 | TAF 1168 |
| 12 | Thy 2 | + | 1.2 | D000617 | lipocortin II |
| 13 | Thy 3 | + | 1.7 | X05615 | thyroglobulin |
| 14 | Thy 5 | + | 2.7 | Novel | Novel-EST matches |
| 15 | Thy 6 | ++ | 3.4 | Novel | Novel-ESTs |
| 16 | Thy 9 | + | 0.6 | M17733 | thymosin beta-4 |
| 17 | Thy 11 | + | 4.2 | Novel | Novel-EST matches |
| 18 | Thy 12 | ++ | 0.8 | U70063 | Acid ceramidase |
| 19 | Thy 14 | ++ | 2.9 | Novel | Novel-EST matches |
| 20 | Thy 15 | ++ | 2.5 | Novel | Novel-EST matches |

Table III

| SEQ ID NO. | Accession NO. | Identity |
|------------|---------------|---|
| 21 | D30612 | Homo sapiens mRNA for repressor protein, partial cds |
| 22 | D86956 | Human mRNA for KIAA0201 gene, complete cds |
| 23 | X65550 | H.sapiens mki67a mRNA (long type) for antigen of monoclonal antibody Ki-67 |
| 24 | X65551 | H.sapiens mki67a mRNA (short type) for antigen of monoclonal antibody Ki-67 |
| 25 | X55039 | Human hCENP-B gene for centromere autoantigen B (CENP-B) |
| 26 | X98893 | H.sapiens mRNA for TBP associated factor (TAFII68) |
| 27 | D00017 | Homo sapiens mRNA for lipocortin II, complete cds |
| 28 | X05615 | Human mRNA for thyroglobulin |
| 29 | M17733 | Human thymosin beta-4 mRNA, complete cds |
| 30 | U70063 | Human acid ceramidase mRNA, complete cds |

Example 3**Clone Reactivity with
Sera from Allogeneic Cancer Patients**

5 The SEREX clones were tested for reactivity
with 52 allogeneic sera from cancer patients (7 rectal,
13 lung, 21 breast, 11 colon) and 10 allogeneic sera
from normal individuals. The procedure was essentially
as the SEREX method described in Example 1, except that
10 'defined' cDNA molecules, i.e., the isolated clones
were being expressed, blotted and screened with
allogeneic sera rather than autologous sera. The
allogeneic sera were treated in the same way the
autologous sera were treated which as described in
15 Example 1. Briefly, XL-1 E Coli cells were grown to OD
1.0, spun down and suspended in 10 ml MgSO₄. 20 ml of
primary phage stock in SM-buffer were added to 100 ml
of bacterial solution. Phage was sorbed for 15 min at
28°C, then 0.5 ml of 2 YT medium and IPTG were added
20 and samples were incubated at 42°C until lysis (6-7
hrs). Afterwards, cell debris was spun down and 2 ml
solution were transferred to Hybond-C filters,
incubated with allogeneic sera samples overnight (sera
1:100) and developed by standard method with anti-human
25 anti-IgG horse radish peroxidase conjugate, stained
with DAB. The level of immunoreactivity was estimated
in arbitrary units, where 4=high signal level, 3=medium
signal level, 2=weak signal, 1= absence of signal. An
average mean of signals for each clone and type of
30 cancer have been calculated, and mean of average signal
for normal sera have been subtracted. Table IV
summarizes the results.

35

Table IV Dot Blot Analysis

| | | C L O N E S | | | | | | | | | | | | | | | | | | | | | | | | |
|----|--------------|---------------|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|---|---|---|--|
| | | ID NO | 1 | 2 | 3 | 5 | 6 | 9 | 11 | 12 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | | | | |
| | | Rectal cancer | | | | | | | | | | | | | | | | | | | | | | | | |
| 5 | Rec1 | 1 | 2 | 1 | 4 | 3 | 1 | 1 | 2 | 1 | 2 | 2 | 3 | 3 | 3 | 3 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | |
| | Rec8 | 1 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 2 | 2 | 3 | 2 | 2 | 3 | 3 | 3 | 2 | 2 | 3 | 3 | 3 | 3 | 3 | 3 | |
| | Rec3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 2 | 2 | 2 | 3 | 3 | 3 | 3 | 3 | 3 | |
| | Rec4 | 2 | 2 | 3 | 3 | 3 | 2 | 3 | 3 | 3 | 2 | 3 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 3 | 3 | 3 | 3 | 3 | 3 | |
| | Rec5 | 4 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 3 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 3 | |
| 10 | Rec6 | 4 | 2 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 2 | 2 | 3 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 3 | |
| | Rec2 | 3 | 2 | 3 | 3 | 3 | 2 | 3 | 3 | 3 | 3 | 3 | 3 | 4 | 3 | 3 | 3 | 2 | 2 | 2 | 2 | 3 | 3 | 3 | 3 | |
| | | 18 | 16 | 18 | 21 | 20 | 16 | 18 | 19 | 17 | 16 | 18 | 20 | 17 | 18 | 16 | 14 | 14 | 17 | 18 | 20 | | | | | |
| | | Lung cancer | | | | | | | | | | | | | | | | | | | | | | | | |
| 15 | Lu2 | 1 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 2 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | |
| | Lu3 | 1 | 3 | 3 | 4 | 3 | 3 | 3 | 3 | 3 | 1 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | |
| | Lu46 | 1 | 2 | 3 | 3 | 3 | 2 | 1 | 1 | 1 | 3 | 2 | 3 | 3 | 3 | 3 | 3 | 3 | 2 | 2 | 2 | 2 | 4 | 4 | 4 | |
| | Lu18 | 3 | 2 | 3 | 4 | 3 | 3 | 3 | 3 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | |
| | Lu24 | 1 | 1 | 1 | 3 | 3 | 3 | 3 | 2 | 2 | 3 | 2 | 2 | 2 | 2 | 3 | 3 | 3 | 2 | 3 | 3 | 4 | 4 | 4 | 4 | |
| 20 | Lu26 | 3 | 2 | 3 | 3 | 3 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | |
| | Lu40 | 1 | 3 | 3 | 3 | 3 | 2 | 3 | 3 | 1 | 2 | 2 | 2 | 2 | 3 | 3 | 2 | 2 | 3 | 3 | 4 | 4 | 4 | 4 | 4 | |
| | Lu44 | 1 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 2 | 2 | 3 | 4 | 4 | 4 | 4 | 4 | |
| | Lu17 | 1 | 3 | 3 | 3 | 3 | 2 | 2 | 3 | 2 | 3 | 3 | 2 | 2 | 3 | 3 | 3 | 3 | 1 | 3 | 4 | 4 | 4 | 4 | 4 | |
| | Lu49 | 3 | 2 | 2 | 3 | 3 | 2 | 3 | 3 | 3 | 2 | 2 | 3 | 2 | 3 | 3 | 3 | 3 | 3 | 2 | 2 | 3 | 4 | 4 | 4 | |
| 25 | Lu4 | 2 | 2 | 2 | 3 | 3 | 2 | 2 | 3 | 2 | 1 | 2 | 3 | 1 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 3 | 4 | 4 | 4 | |
| | Lu47 | 2 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | |
| | Lu50 | 2 | 1 | 1 | 3 | 3 | 1 | 1 | 2 | 2 | 1 | 2 | 2 | 3 | 3 | 3 | 3 | 1 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | |
| | | 22 | 30 | 33 | 41 | 39 | 31 | 32 | 34 | 29 | 29 | 30 | 32 | 30 | 35 | 34 | 34 | 28 | 33 | 34 | 42 | | | | | |
| | | Breast cancer | | | | | | | | | | | | | | | | | | | | | | | | |
| 30 | Br2 | 3 | 2 | 1 | 3 | 2 | 3 | 2 | 2 | 3 | 3 | 2 | 2 | 3 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 3 | 4 | 4 | 4 | |
| | Br15 | 4 | 2 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 2 | 4 | 2 | 4 | 3 | 2 | 2 | 2 | 3 | 3 | 4 | 4 | 4 | 4 | 4 | |
| | Br8 | 4 | 1 | 1 | 2 | 2 | 1 | 2 | 2 | 3 | 1 | 1 | 3 | 3 | 2 | 2 | 2 | 2 | 1 | 1 | 3 | 4 | 4 | 4 | 4 | |
| | Br1 | 3 | 1 | 2 | 2 | 2 | 2 | 1 | 3 | 1 | 2 | 2 | 3 | 3 | 2 | 2 | 1 | 1 | 2 | 1 | 2 | 3 | 4 | 4 | 4 | |
| | Br9 | 2 | 2 | 2 | 2 | 3 | 3 | 3 | 3 | 1 | 3 | 2 | 3 | 2 | 2 | 2 | 2 | 2 | 2 | 1 | 2 | 1 | 3 | 4 | 4 | |
| 35 | Br3 | 2 | 1 | 3 | 2 | 3 | 3 | 3 | 2 | 2 | 2 | 1 | 3 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 3 | 4 | 4 | 4 | 4 | |
| | Br10 | 3 | 2 | 4 | 3 | 3 | 3 | 1 | 4 | 2 | 2 | 3 | 4 | 4 | 3 | 3 | 3 | 2 | 2 | 2 | 2 | 3 | 4 | 4 | 4 | |
| | Br17 | 3 | 3 | 3 | 3 | 3 | 2 | 3 | 3 | 3 | 2 | 3 | 3 | 3 | 3 | 3 | 1 | 1 | 3 | 3 | 3 | 4 | 4 | 4 | 4 | |
| | Br16 | 1 | 1 | 1 | 1 | 2 | 2 | 1 | 2 | 1 | 2 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 2 | 3 | 4 | 4 | 4 | |
| | Br4 | 2 | 2 | 2 | 1 | 2 | 2 | 2 | 2 | 1 | 1 | 1 | 2 | 2 | 2 | 2 | 2 | 1 | 1 | 1 | 1 | 2 | 3 | 4 | 4 | |
| 40 | Br6 | 3 | 2 | 2 | 1 | 2 | 1 | 2 | 2 | 1 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 3 | 4 | 4 | 4 | |
| | Br14 | 2 | 2 | 1 | 1 | 4 | 3 | 3 | 3 | 2 | 2 | 1 | 3 | 3 | 3 | 3 | 3 | 3 | 2 | 2 | 3 | 4 | 4 | 4 | 4 | |
| | Br5 | 3 | 3 | 3 | 2 | 4 | 3 | 3 | 3 | 2 | 2 | 2 | 3 | 3 | 3 | 3 | 3 | 3 | 1 | 1 | 2 | 3 | 4 | 4 | 4 | |
| | Br20 | 1 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 1 | 2 | 2 | 1 | 2 | 2 | 1 | 2 | 1 | 1 | 1 | 1 | 2 | 3 | 4 | 4 | |
| | Br12 | 3 | 1 | 3 | 2 | 3 | 3 | 2 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 2 | 2 | 2 | 3 | 2 | 2 | 3 | 4 | 4 | 4 | |
| 45 | Br19 | 3 | 3 | 3 | 2 | 3 | 3 | 2 | 3 | 2 | 2 | 2 | 3 | 3 | 1 | 3 | 3 | 1 | 1 | 1 | 1 | 2 | 3 | 4 | 4 | |
| | Br18 | 3 | 3 | 3 | 2 | 3 | 3 | 2 | 2 | 1 | 1 | 2 | 2 | 2 | 2 | 2 | 3 | 1 | 1 | 1 | 1 | 3 | 4 | 4 | 4 | |
| | Br11 | 2 | 1 | 2 | 1 | 3 | 2 | 2 | 2 | 1 | 1 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 1 | 1 | 2 | 3 | 4 | 4 | |
| | Br248 | 1 | 1 | 2 | 2 | 2 | 2 | 3 | 2 | 4 | 2 | 3 | 3 | 2 | 3 | 3 | 1 | 1 | 3 | 3 | 4 | 4 | 4 | 4 | 4 | |
| | Br257 | 1 | 2 | 3 | 3 | 3 | 3 | 3 | 3 | 4 | 1 | 3 | 2 | 3 | 4 | 4 | 4 | 3 | 3 | 3 | 4 | 4 | 4 | 4 | 4 | |
| 50 | Br263 | 1 | 2 | 2 | 3 | 3 | 2 | 4 | 3 | 4 | 2 | 2 | 1 | 2 | 2 | 2 | 2 | 1 | 1 | 2 | 3 | 3 | 4 | 4 | 4 | |
| | | 50 | 39 | 48 | 43 | 57 | 51 | 49 | 54 | 45 | 40 | 44 | 51 | 54 | 48 | 48 | 42 | 34 | 37 | 43 | 56 | | | | | |
| | Colon cancer | | | | | | | | | | | | | | | | | | | | | | | | | |
| | Co5 | 4 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 2 | 2 | 3 | 3 | 3 | 3 | 3 | 1 | 3 | 3 | 3 | 4 | 4 | 4 | 4 | |
| | Co30 | 3 | 2 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 2 | 2 | 3 | 3 | 3 | 3 | 3 | 2 | 3 | 3 | 3 | 4 | 4 | 4 | 4 | |
| 55 | Co17(?) | 4 | 2 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 2 | 3 | 3 | 3 | 3 | 3 | 3 | 2 | 2 | 3 | 3 | 3 | 4 | 4 | 4 | |
| | Co37 | 3 | 1 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 3 | 3 | 2 | 2 | 2 | 1 | 1 | 2 | 2 | 3 | 4 | 4 | 4 | |
| | Co33 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 2 | 2 | 3 | 3 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 3 | 4 | 4 | 4 | |

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| | | | | | | | | | | | | | | | | | | | | | |
|------------|--------|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|
| 5 | Co4 | 4 | 2 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 2 | 2 | 3 | 3 | 3 |
| | Co34 | 3 | 2 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 2 | 2 | 3 | 3 | 3 |
| | Co36 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 2 | 2 | 3 | 3 | 3 |
| | Co2 | 2 | 2 | 2 | 2 | 3 | 3 | 2 | 2 | 2 | 2 | 3 | 3 | 3 | 3 | 3 | 1 | 1 | 2 | 2 | 3 |
| | Co3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 2 | 2 | 2 | 3 | 3 | 3 |
| | Co32 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 1 | 2 | 2 | 3 | 2 | 2 | 2 | 1 | 1 | 3 | 3 | 3 |
| CL O N E S | | | | | | | | | | | | | | | | | | | | | |
| 10 | ID | 1 | 2 | 3 | 5 | 6 | 9 | 11 | 12 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 |
| | Normal | | | | | | | | | | | | | | | | | | | | |
| 15 | sera | | | | | | | | | | | | | | | | | | | | |
| | No10 | 3 | 1 | 1 | 2 | 1 | 2 | 2 | 1 | 2 | 2 | 3 | 3 | 2 | 3 | 2 | 2 | 2 | 2 | 2 | 2 |
| | No8 | 1 | 1 | 3 | 2 | 2 | 2 | 2 | 2 | 2 | | | | | | | | | | | |
| | No5 | 1 | 2 | 2 | 3 | 1 | 1 | 3 | 2 | 2 | 1 | 1 | 2 | 2 | 1 | 2 | 2 | 3 | 1 | 2 | 2 |
| | No22 | 2 | 2 | 2 | 1 | 2 | 2 | 3 | 3 | 1 | 3 | 2 | 2 | 2 | 1 | 4 | 1 | 3 | 1 | 2 | 2 |
| | No13 | 1 | 1 | 2 | 2 | 1 | 2 | 3 | 2 | 1 | 1 | 1 | 1 | 1 | 1 | 2 | 1 | 2 | 1 | 1 | 1 |
| 20 | No3 | 1 | 2 | 3 | 2 | 1 | 2 | 2 | 1 | 1 | 1 | 1 | 2 | 3 | 2 | 3 | 2 | 3 | 1 | 2 | 2 |
| | No21 | 1 | 2 | 3 | 3 | 2 | 2 | 2 | 2 | 2 | 1 | 1 | 2 | 2 | 1 | 3 | 2 | 2 | 1 | 2 | 2 |
| | No1 | 2 | 2 | 2 | 1 | 1 | 2 | 2 | 2 | 2 | 1 | 1 | 1 | 3 | 1 | 2 | 1 | 2 | 1 | 1 | 1 |
| | No2 | 1 | 1 | 2 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 2 | 3 | 1 | 1 | 2 | 2 | 1 | 2 | 2 |
| | No15 | 2 | 2 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 2 | 3 | 1 | 2 | 1 | 2 | 1 | 1 | 1 |
| | | 15 | 16 | 21 | 18 | 13 | 17 | 21 | 17 | 15 | 12 | 12 | 17 | 21 | 12 | 21 | 14 | 21 | 10 | 15 | 15 |

All sera scoring 4 or 3 were classed as positive and the results of the dot blotting were summarized in Table V.

5 **Table V Clone Reactivity with Allogenic Sera**

| | ID | Clone | SEQ ID NO | Allogenic cancer sera | | | | |
|----|----|-------|-----------|-----------------------|----------------|------------------|-----------------|------------------|
| | | | | Rectal (n=7) | Lung (n=13) | Breast (n=21) | Colon (n=11) | Normal (n=10) |
| 10 | 1 | Thy1 | 11 | 4 | 3 | 11 | 10 | 1 |
| | 2 | Thy2 | 12 | 2 | 6 | 4 | 5 | 0 |
| | 3 | Thy3 | 13 | 5 | 9 | 9 | 9 | 9 |
| | 5 | Thy5 | 14 | 6 | 13 | 6 | 9 | 2 |
| | 6 | Thy6 | 15 | 6 | 13 | 13 | 10 | 0 |
| 15 | 9 | Thy9 | 16 | 3 | 6 | 11 | 10 | 0 |
| | 11 | Thy11 | 17 | 5 | 8 | 9 | 9 | 3 |
| | 12 | Thy12 | 18 | 5 | 9 | 11 | 9 | 1 |
| | 14 | Thy14 | 19 | 4 | 5 | 8 | 8 | 0 |
| | 15 | Thy15 | 20 | 2 | 6 | 3 | 4 | 1 |
| 20 | 16 | Mel1 | 1 | 4 | 4 | 6 | 6 | 1 |
| | 17 | Mel2 | 2 | 5 | 6 | 11 | 11 | 1 |
| | 18 | Mel3 | 3 | 3 | 5 | 11 | 10 | 4 |
| | 19 | Mel4 | 4 | 4 | 9 | 7 | 7 | 1 |
| 25 | 20 | Mel5 | 5 | 2 | 8 | 7 | 7 | 3 |
| | 21 | Mel6 | 6 | 0 | 8 | 6 | 2 | 0 |
| | 22 | Mel7 | 7 | 0 | 4 | 2 | 0 | 3 |
| | 23 | Mel8 | 8 | 3 | 7 | 4 | 8 | 0 |
| | 24 | Mel9 | 9 | 4 | 8 | 7 | 8 | 0 |
| | 25 | Mel10 | 10 | 6 | 11 | 13 | 10 | 0 |

Based on the data in Table V, the mean of the intensity values for each cancer sera type was calculated for each clone. The mean of the intensity values for each normal sera type was calculated For each clone. The
5 difference between the cancer sera and normal sera is presented in Table VI. A value over 1.0 indicates a specific recognition of the clone by the type of cancer sera.

So for instance, SEQ ID No's 4, 8, 9, 10, which
10 represent sequences of Ki-67, are specifically recognized by serum antibodies from rectal, lung, breast and colon cancer patients. Ki-67 is a marker of proliferation used in immunohistochemistry. The present invention has shown for the first time the association of this antigen with
15 cancer.

Table VI Specific Clone reactivity with allogenic cancer sera

| | ID | Clone | SEQ ID NO | Allogenic cancer sera | | | |
|----|----|-------|-----------|-----------------------|----------------|------------------|-----------------|
| | | | | Rectal (n=7) | Lung (n=13) | Breast (n=21) | Colon (n=11) |
| 5 | 1 | Thy1 | 11 | 1.07 | 0.19 | 0.88 | 1.68 |
| | 2 | Thy2 | 12 | 0.69 | 0.71 | 0.26 | 0.76 |
| | 3 | Thy3 | 13 | 0.47 | 0.44 | 0.19 | 0.72 |
| 10 | 5 | Thy5 | 14 | 1.2 | 1.35 | 0.24 | 1.02 |
| | 6 | Thy6 | 15 | 1.55 | 1.7 | 1.41 | 1.61 |
| | 9 | Thy9 | 16 | 0.59 | 0.68 | 0.73 | 1.21 |
| | 11 | Thy11 | 17 | 0.47 | 0.36 | 0.23 | 0.72 |
| | 12 | Thy12 | 18 | 1.01 | 0.92 | 0.87 | 1.12 |
| 15 | 14 | Thy14 | 19 | 0.92 | 0.73 | 0.64 | 1.14 |
| | 15 | Thy15 | 20 | 1.09 | 1.03 | 0.7 | 1.16 |
| 20 | 16 | Mel1 | 1 | 1.37 | 1.11 | 0.9 | 1.35 |
| | 17 | Mel2 | 2 | 1.16 | 0.76 | 0.73 | 1.3 |
| | 18 | Mel3 | 3 | 0.32 | 0.21 | 0.47 | 0.81 |
| | 19 | Mel4 | 4 | 1.37 | 1.49 | 1.09 | 1.44 |
| | 20 | Mel5 | 5 | 0.91 | 0.52 | 0.19 | 0.54 |
| | 21 | Mel6 | 6 | 0.6 | 1.22 | 0.6 | 0.6 |
| 25 | 22 | Mel7 | 7 | 0 | 0.05 | 0 | 0 |
| | 23 | Mel8 | 8 | 1.42 | 1.54 | 0.76 | 1.64 |
| | 24 | Mel9 | 9 | 1.07 | 1.12 | 0.54 | 1.23 |
| | 25 | Mel10 | 10 | 1.36 | 1.73 | 1.17 | 1.41 |

Example 3**Reactivity of a Fragment of Ki67
Recombinantly Expressed in Bacteria
With Allogenic Sera from Cancer Patients**

5

A 0.5 kB sequence of Mel-9 clone was amplified by PCR, using Vent polymerase and a pair of specific primers. The primers used are:

10

Oligo N1, Ki67 sense, Nhe, 6His, 5610
ATTGCTAGCCACCACCACCACCACAACTGGACCCAGCAGCAAGTGTAAAC
(SEQ ID NO:31); and
Oligo N2, Ki67 antisense, EcoRI, 6420
CGGGAATTCCTATAGAGCCTCAGCCTTTTCCTTAGG (SEQ ID NO: 32)

15

Amplified cDNA fragment of Ki67 was subcloned into pET23d in a correct reading frame with the His-tag epitope. Expression of recombinant His-tag/Ki67 was carried out in DE3 pLysS cells in the presence of 1 mM IPTG. Recombinant protein had a predicted molecular weight (about 21 kDa) and was purified nearly to homogeneity by affinity chromatography on Talon Sepharose. Purified His-tag/Ki67 was used for heterologous screening of sera from healthy individuals and cancer patients.

25

Highly purified recombinant Ki67 was coupled to 96-well immunoassay plates (0.1-1 mkg per well). Non-specific binding of sera's IgG to plates was blocked by BSA. Binding of recombinant Ki-67 by specific antibodies present in normal and cancer sera was measured by ELISA using standard techniques. Four experiments were done. In each experiment, each sample of normal or cancer sera was tested against recombinant Ki-67. The mean values for corresponding sera types were calculated in each experiment and averages for normal and cancer sera were compared to determine differences. The difference in the measured intensity reflects the

30

35

difference in the amount of specific antibodies between cancer and normal sera.

Table VII presents the results. The results of this study indicate that sera from lung and breast cancer patients show increased immunoreactivity towards recombinant Ki67. The differences between the cancer sera and normal sera in immunoreactivity towards recombinant Ki67 were considered valid if p-value was less than 0.05. Statistical analysis indicated that significant differences were seen with lung and breast cancer sera, indicating that these cancer seras contained greater amounts of Ki-67 specific antibodies compared to normal sera.

Table VII

ELIZA: Recombinant Ki-67 screened with allogenic cancer and normal sera

| | Exp | Sera Compared | Difference | Statistically Significant |
|----|-------|---------------|------------|---------------------------|
| 20 | exp 1 | N1 vs. LU1 | + | Yes |
| | exp 1 | N1 vs. BR1 | + | Yes |
| | exp 1 | N1 vs. THY1 | + | No |
| | exp 2 | N2 vs. LU2 | + | Yes |
| 25 | exp 2 | N2 vs. CO2 | + | No |
| | exp 3 | N3 vs. LU3 | + | Yes |
| | exp 3 | N3 vs. BR3 | + | Yes |
| | exp 3 | N3 vs. THY3 | + | No |
| 30 | exp 4 | N4 vs. LU4 | + | Yes |
| | exp 4 | N4 vs. BR4 | + | Yes |

35

WHAT IS CLAIMED IS:

1. An isolated nucleic acid molecule or a part thereof, wherein said nucleic acid molecule has a sequence as set forth in any one of SEQ ID NOS: 3, 7, 14, 17, 19 or 20.

2. The isolated nucleic acid molecule or a part thereof of claim 1, wherein said nucleic acid molecule has a sequence as set forth in SEQ ID NO: 3.

3. The isolated nucleic acid molecule or a part thereof of claim 1, wherein said nucleic acid molecule has a sequence as set forth in SEQ ID NO: 7.

4. The isolated nucleic acid molecule or a part thereof of claim 1, wherein said nucleic acid molecule has a sequence as set forth in SEQ ID NO: 14.

5. The isolated nucleic acid molecule or a part thereof of claim 1, wherein said nucleic acid molecule has a sequence as set forth in SEQ ID NO: 15.

6. The isolated nucleic acid molecule or a part thereof of claim 1, wherein said nucleic acid molecule has a sequence as set forth in SEQ ID NO: 17.

7. The isolated nucleic acid molecule or a part thereof of claim 1, wherein said nucleic acid molecule has a sequence as set forth in SEQ ID NO: 19.

8. The isolated nucleic acid molecule or a part thereof of claim 1, wherein said nucleic acid molecule has a sequence as set forth in SEQ ID NO: 20.

9. An isolated nucleic acid molecule comprising a nucleotide sequence, the complementary sequence of which hybridizes under stringent conditions to at least one nucleic acid molecule of SEQ ID NOS: 3, 7, 14-15, 17 or 19-20.

10. An isolated protein encoded by the isolated nucleic acid molecule or a part thereof of claim 1.

11. An isolated antibody specific for a protein encoded by the nucleic acid molecule or a part thereof of claim 1.

12. An expression vector comprising the nucleic acid molecule or a part thereof of claim 1, operably linked to a promoter to effect the expression of a protein encoded by said nucleic acid molecule or a part thereof.

13. A cell, transformed or tranfected with the isolated nucleic acid molecule or a part thereof of claim 1.

14. A cell, transformed or tranfected with the expression vector of claim 12.

15. The cell of claim 14, wherein said cell is an antigen presenting cell having on the surface, a complex of an MHC molecule and a peptide, said peptide being encoded by a fragment of said nucleic acid molecule.

16. An isolated peptide/HLA complex, wherein said peptide is encoded by a fragment of any one of SEQ ID NOS: 3, 7, 14-15, 17 or 19-20.

17. A method for diagnosing a pathological condition in a patient, wherein said condition is characterized by an abnormal expression of at least one nucleic acid molecule of SEQ ID NOS: 21-30 or a nucleic acid sequence comprising any one of SEQ ID NO: 3, 7, 14-15, 17 or 19-20, said method comprising the steps of:

- (i) obtaining a sample from said patient;
- (ii) assessing the expression of said nucleic acid molecule in said sample; and
- (iii) determining the expression of said nucleic acid molecule as abnormal thereby diagnosing said pathological condition.

18. The method of claim 17, wherein said pathological condition is selected from the group consisting of melanoma, the presence of a thyroid tumor, rectal cancer, lung cancer, breast cancer and colon cancer.

19. The method of Claim 18, wherein said pathological condition is melanoma and wherein said nucleic acid molecule is any one of SEQ ID NO: 21-25, or a nucleic acid sequence comprising SEQ ID NO: 3 or 7.

20. The method of Claim 18, wherein said pathological condition is characterized by the presence of a thyroid tumor and wherein said nucleic acid molecule is any one of SEQ ID NOS: 26-30, or a nucleotide sequence comprising any one of SEQ ID NOS: 14-15, 17 or 19-20.

21. The method of Claim 18, wherein said pathological condition is rectal cancer and wherein said nucleic acid molecule is any one of SEQ ID NOS:

21-24, 26 or 30, or a nucleotide sequence comprising any one of SEQ ID NOS: 14-15 or 20.

22. The method of Claim 18, wherein said pathological condition is lung cancer and wherein said nucleic acid molecule is any one of SEQ ID NOS: 21 or 23-25, or a nucleotide sequence comprising any one of SEQ ID NOS: 14-15 or 20.

23. The method of Claim 18, wherein said pathological condition is breast cancer and wherein said nucleic acid molecule is any one of SEQ ID NOS: 23-24, or a nucleotide sequence comprising SEQ ID NO: 15.

24. The method of Claim 18, wherein said pathological condition is colon cancer and wherein said nucleic acid molecule is any one of SEQ ID NOS: 21-24, 26 or 29-30, or a nucleotide sequence comprising SEQ ID NO: 14-15 or 19-20.

25. The method of claim 18, wherein the expression of said nucleic acid molecule is assessed by assaying the level of mRNA of said nucleic acid molecule.

26. The method of claim 18, wherein the expression of said nucleic acid molecule is assessed by assaying the level of a protein encoded by said nucleic acid molecule or parts thereof.

27. The method of claim 18, wherein the expression of said nucleic acid molecule is assessed by assaying the level of an antibody in the serum that is specific for a protein encoded by said nucleic acid molecule or parts thereof.

28. The method of claim 18, wherein the expression of said nucleic acid molecule is assessed by assaying a cell expressing an MHC/peptide complex and wherein said peptide is encoded by a fragment of said nucleic acid molecule.

29. A composition comprising a carrier and an antisense DNA of a nucleic acid molecule or a part thereof, wherein said nucleic acid molecule is any one of SEQ ID NOS: 21-30, or a nucleic acid sequence comprising any one of SEQ ID NO: 3, 7, 14-15, 17 or 19-20.

30. A composition comprising a carrier and a protein encoded by a nucleic acid molecule or a part thereof, wherein said nucleic acid molecule is any one of SEQ ID NOS: 21-30, or a nucleic acid sequence comprising any one of SEQ ID NO: 3, 7, 14-15, 17 or 19-20.

31. A composition comprising a carrier and an antibody directed against a protein encoded by a nucleic acid molecule or a part thereof, wherein said nucleic acid molecule is any one of SEQ ID NOS: 21-30, or a nucleic acid sequence comprising any one of SEQ ID NO: 3, 7, 14-15, 17 or 19-20.

32. A composition comprising an immunogenic cell and a carrier, wherein said cell expresses a peptide complexed with an MHC molecule, said peptide being encoded by a fragment of a nucleic acid molecule, and wherein said nucleic acid molecule is any one of SEQ ID NOS: 14-15, 17 or 19-20.

33. A method for treating a patient afflicted with a pathological condition, wherein said

condition is characterized by an abnormal expression of at least one nucleic acid molecule of SEQ ID NOS: 21-30 or a nucleic acid sequence comprising any one of SEQ ID NO: 3, 7, 14-15, 17 or 19-20; said method comprising administering to said patient a therapeutically effective amount of at least one of: an antisense DNA of said nucleic acid molecule or part thereof, a protein encoded by said nucleic acid molecule or part thereof, an antibody specific for a protein encoded by said nucleic acid molecule or part thereof, or a cell expressing a MHC/peptide complex wherein said peptide is encoded by a fragment of said nucleic acid molecule.

34. The method of claim 33, wherein said pathological condition is selected from the group consisting of melanoma, the presence of a thyroid tumor, rectal cancer, lung cancer, breast cancer and colon cancer.

35. The method of claim 34, wherein said pathological condition is melanoma and wherein said nucleic acid molecule is any one of SEQ ID NOS: 21-25, or a nucleic acid sequence comprising SEQ ID NO: 3 or 7.

36. The method of claim 34, wherein said pathological condition is characterized by the presence of a thyroid tumor and wherein said nucleic acid molecule is any one of SEQ ID NOS: 26-30, or a nucleic acid sequence comprising any one of SEQ ID NOS: 14-15, 17 or 19-20.

37. The method of Claim 34, wherein said pathological condition is rectal cancer and wherein said nucleic acid molecule is any one of SEQ ID NOS:

21-24, 26 or 30, or a nucleotide sequence comprising any one of SEQ ID NOS: 14-15 or 20.

38. The method of Claim 34, wherein said pathological condition is lung cancer and wherein said nucleic acid molecule is any one of SEQ ID NOS: 21 or 23-25, or a nucleotide sequence comprising any one of SEQ ID NOS: 14-15 or 20.

39. The method of Claim 34, wherein said pathological condition is breast cancer and wherein said nucleic acid molecule is any one of SEQ ID NOS: 23-24, or a nucleotide sequence comprising SEQ ID NO: 15.

40. The method of Claim 34, wherein said pathological condition is colon cancer and wherein said nucleic acid molecule is any one of SEQ ID NOS: 21-24, 26 or 29-30, or a nucleotide sequence comprising SEQ ID NO: 14-15 or 19-20.

41. A method for treating a subject afflicted with a pathological condition, wherein said condition is characterized by an abnormal expression of at least one nucleic acid molecule of SEQ ID NOS: 21-30 or a nucleic acid sequence comprising SEQ ID NO: 3, 7, 14-15, 17 or 19-20, said method comprising:

(i) removing an immuno-reactive cell containing sample from said subject,

(ii) contacting the immuno-reactive cell containing sample with immunogenic cells expressing a peptide encoded by a fragment of said nucleic acid molecule complexed with an MHC molecule;

(iii) selecting the cytolytic T cells that are specific for said peptide; and

(iv) introducing a therapeutic effective amount of the cytolytic T cells produced from step (iii) to said subject thereby alleviating said condition.

42. The method of claim 41, wherein said pathological condition is one selected from the group consisting of melanoma, the presence of a thyroid tumor, rectal cancer, lung cancer, breast cancer and colon cancer.

43. The method of claim 42, wherein said pathological condition is melanoma and wherein said nucleic acid molecule is any one of SEQ ID NOS: 21-25, or a nucleic acid sequence comprising SEQ ID NO: 3 or 7.

44. The method of claim 42, wherein said pathological condition is characterized by the presence of a thyroid tumor and wherein said nucleic acid molecule is any one of SEQ ID NOS: 26-30, or a nucleic acid sequence comprising any one of SEQ ID NOS: 14-15, 17 or 19-20.

45. The method of Claim 42, wherein said pathological condition is rectal cancer and wherein said nucleic acid molecule is any one of SEQ ID NOS: 21-24, 26 or 30, or a nucleotide sequence comprising any one of SEQ ID NOS: 14-15 or 20.

46. The method of Claim 42, wherein said pathological condition is lung cancer and wherein said nucleic acid molecule is any one of SEQ ID NOS: 21 or 23-25, or a nucleotide sequence comprising any one of SEQ ID NOS: 14-15 or 20.

47. The method of Claim 42, wherein said pathological condition is breast cancer and wherein said nucleic acid molecule is any one of SEQ ID NOS: 23-24, or a nucleotide sequence comprising SEQ ID NO: 15.

48. The method of Claim 42, wherein said pathological condition is colon cancer and wherein said nucleic acid molecule is any one of SEQ ID NOS: 21-24, 26 or 29-30, or a nucleotide sequence comprising SEQ ID NO: 14-15 or 19-20.

49. A method of identifying the association of a pathological condition with an abnormal expression of a nucleic acid molecule, wherein said nucleic acid molecule is any one of SEQ ID NOS: 21-30 or a nucleic acid sequence comprising SEQ ID NO: 3, 7, 14-15, 17 or 19-20, said method comprising:

obtaining the serum from a patient suffering said pathological condition; and

detecting the presence of an antibody in said serum specific for an antigen encoded by said nucleic acid molecule, as indicative of an association of said pathological condition with the abnormal expression of said nucleic acid molecule.

50. The method of claim 49, wherein said nucleic acid molecule is SEQ ID NO: 23 or 24.

51. The method of claim 49, wherein said pathological condition is a cancer.

52. The method of claim 49, wherein the detection is carried out using a SEREX screening assay.

SEQ ID NO: 1 (Me11)

5 TGTNCAANGGGGNTNAGTGGTNACNGNCATGGGTACNNGCCTNTTCCC
NNNGCNCCNGNNATATTGNGTGCANGNCGCANTNTTTNGNANANGCAGCN
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10 NTGGCTACAGACCNTGNTGNGGCCANACCNTGCAGGCGCCTCGGGAAGCG
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15 TGGGCAGCCGGCACCCGGCACC ACTTTGGCGNGCGTCCTGCTTCGCCCT
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AAA

20

SEQ ID NO: 2 (Me12)

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30 ATATTGATGAGTCTGAAATGAAAAAGTGGAGAAGTCTGTTAATGAAGTG
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SEQ ID NO: 3 (Me13)

5 TGGGNTTTTCCCCCTTTTTTNGNAACCCCNNTTTCNTNCCCCNNTTGT
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10 CCGNNGNAGGTCCNCNNTTGGCCCCCTNCAAGGGTNGGNGCCCCNCCCC
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TTCCCTTTGGNTTTGCCCCTNGGTTTTTTTTCCCGGTTTGGGGNTTNCCA
GGGGCCCCCCCCCTNGGAGTTNCCCAGGGGGGTTCNNTTNGGNCNNTN
15 CCGGNCCCCTNCCCTTCTCCCNNTTNGNNGGNCNCCCTTTTTGGCCGG
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NNTTNGTTTNNATNAANTTTNCCNCTCCCCCTTTTNGGGGNNGACNTTT
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20 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
A

SEQ ID NO: 4 (Me14)

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30 GAGGCGCAAAAATGAAAAGTACTNTAGCAATTGTGAGCGGACAACAATT
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5 ACACCATCAGTAGGGAAAGCTATGGACACACCCAAACCAGCAGGAGGTGA
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TGCCAGGAAATTTACCTGGCAGCAAAAGATGGCCACAAACTCCTAAGGAA
AAGGCCCAGGC

10

SEQ ID NO: 5 (Me15)

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15 GTCTTGNAAACAGGCCCCGGTTNACTTTGGCCGGGGCCCNNGGGGTGA
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20 GCCATCCACGTCAGGTCTTTGGTGGGGGGACCCCAAAGCCATTTTGGGAA
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25 TTCCAAGAGGCCCCCACCCTGGAAGTAACCAAGGGCGNTTCCTTGTGGG
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30 AA

SEQ ID NO: 6 (Me16)

WO 00/50595

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5 GTCAGCCTCATTGCNTGCTTATTGCNTCTTCTCAGAATCCTCTTTCNTC
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10 CCAGAAGAAGGTCCAGCCTAGGCCCCCTGCAAGGCTGGCAGCCCCACCC
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15 GCAGGCCCCATGCCTCTCCTCCCTCTCTGGCAGGGCCCCATCCTGGGCAG
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20

SEQ ID NO: 7. (Me17)

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30 TNGGTNCCTTNGGCCNGGTTTNNCCCCNNCCTTGNTTTGGGNCCCCC
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WO 00/50595

5 TNCCCTTTCCCTCCCCNTTTGGNCGGGCCCCCTTNTNGGCCGGGGGGCCCTTG
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AAA
AAA
AAAAA

10 SEQ ID NO: 8 (Me18)

15 TGAAAAGGGGCNTTNAANGGCNTTTAAGGAATTTTGCAAAGCCAGATTG
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20 AACTGCAAAACAGAACTGGACCCAGCAGCAAGTGTAAGTGGTAGCAAGA
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25 GCAGACGTAGAGGAAGAATCCTTAGCACTCAGGAAACGAACACCATCAGT
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30

SEQ ID NO:9 (Me19)

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5 TGGATGATAACGAGGCGCAAAAANTGAAAAGTACTTCTTGCAATTGTGAG
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15 TAGGGAAAGCTATGGACACACCCAAACCAGCAGGAGGTGATGAGAAAGAC
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20 SEQ ID NO: 10 (Mel10)

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5 AAATTTACCTGGCAGCAAAAGATGGCCACAACTCCTAAGGAAAAGGCC
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SEQ ID NO: 11 (Thy1)

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15 TCGTTGGAATATTCATGGCGTATTTTGGATGATAACGAGGCGCAAAAAT
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20 AGACCGTGGTGGTGGCAGTGGCTACGGTGGAGACCGAAGTGGAGNNTATG
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25 TTTCCCTCGTGGCCTCTTCTTGGGTGTGAAATTAAGTGACATTTGGATTTT
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30 SEQ ID NO: 12 (Thy2)
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5 CTGGAGTGAAGAGGAAAGGAACTGATGTTCCCAAGTGGATCAGCATCATG
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15

SEQ ID NO: 13 (Thy3)

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SEQ ID NO: 14 (Thy5)

5

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SEQ ID NO: 15 (Thy6)

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GACAAGAATATGAAACAAAATTGAAAGGATTGATGCCAGCATCCCTAAGA
30 CAAGAACTTGAAGACACCATTTCTCCCTAAAATCACAGGTTAATTTTCT
GCAAAAGAGAGCTTCCATCTTCAGGAAGAACTGACTACATATCAAGGCA
GAAGGTAAC TGACGAGAGAATGCAACGGATGCAATTTCCAGGCTGTGCT
GTGGACTTCTTCCAGCAGGTTTGAAGATTTGGATATTGTAACTGTGAGA
TCAGTGGCATTTTTTTAAATCCTTAAATGTAATTAAGATCATAAAACATG

CATCATTTCATAAAAAAAAAAAAAAAAAA

SEQ ID NO: 16 (Thy9)

5 CGGGAATNTCGNTANGTCGAACTGAGGAGACAGAGACGCAAGAGAAAAAT
CCACTGCCTTCCAAAGAAACGATTGAACAGGAGAAGCAAGCAGGCGAATC
GTAATGAGGCGTGCGCCGCCAATATGCACTGTACATTCCACAAGCATTTGC
CTTCTTATTTTACTTCTTTTAGCTGTTTAACTTTGTAAGATGCAAAGAGG
TTGGATCAAGTTTAAATGACTGTGCTGCCCCCTTTCACATCAAAGAACTAC
10 TGACAACGAAGGCCGCGCCTGCCTTTCCCATCTGTCTATCTATCTGGCTG
GCAGGGAAGGAAAGAACTTGCATGTTGGTGAAGGAAGAAGTGGGGTGGAA
GAAGTGGGGTGGGACGACAGTGAAA

15 SEQ ID NO: 17 (Thy11)

TCGGAACAGCNAACAAAGACCATGTCAAGGTCCCAAAGCCCACGGGGGTG
AAGAAGGGATGGCAGNGNGNATATGCAGTCGTCTGTGACTGCAAGCTCTT
CNTGTATGATCTGCNTGAAGGAAAATCCACCCAGCCTGGTGTCAATTGCGA
20 GCCAAGTCTTGGATCTCAGAGATGACGAGTTTCCGTGAGNTCAGTCCTG
GCCTCAGATGCATTCATGNTACACGCCGAGATATCCATGTATATTCAGG
GTGACGGCCTCTCTCTTAGGTGCACCTTNTAAGACCAGCTCTNTGCTCAT
TNTGACNGAAAATGAGAATGAAAAGAGGAAGTGGG

25

SEQ ID NO: 18 (Thy12)

GCTCCGGAAATTTTGGACGGGNCTTTTTTTTTTTTTTCTCGGGGAAGCG
30 GCNCCCATTTGTGTTTGTACCCCGGAATTCGGCNACGGGGACCAAAA
TTGAAGTTGGACAAACGGTTCTTTGCACAAATTGACGTACCATTTTCACA
GTTTAATTCGTGAAGGTTTGGAAAGGTTAACCANGTTCTTATTAGTACTT
TTCATAAGCAGTTGGATTTTCTGAAAAATACAGTAACATAATTTTGTAGTA
ACTTACTTAAAATTTCTTTAAACTCCCTATCAATCTGAAGAACAACATA

AAAACCTGTTTATTACATGAATGCTACTTATGAGAATTTAAAATATGGGT
TCACTTCCTATTTTCCACAAGTCTTTGACTTGTTTATTTACTAAATTAAC
AGAACGTGGGATGCAGTTTTTTAAGTTAGCAACTTCCTTAGGGTTACTGG
GAAGTAGAGTAATTATGAAAAAGGGAACACTTCAATTATTGTATAAAAGA
5 TTGCTTTGCATACTGATTACTTCTTGAACCCCAAAAAGTGCTATTTAGAG
GCAAGGGCCCATTTTGTGCCCATTAAGAAATATACAGGTGAATGTCTG
TCTCATCCCTCTAATCATATGTAATAAAATTATATCGCTGTCAATAACAG
CAAAGATAATGATATATTAATTTTAACAGCAGTTAGAACCAGAAGGAAAA
GGCTGTTATACAGAAAAACATACAAATATGTAGGTAGAAGTGAAAACTG
10 AAGAATGTGGAGTGTTTACTGTCCCGTTACTCACACAGACGTGCTGGATT
CAACACCCACGCTGAATCTCCATTTATTCCACGGAGGTGGAGTTCACCAT
GGTTCGACTGCCCACCAGATCCCCAAATGTCAAAGTGAAACAAAACTCAG
TGAAT

15

SEQ ID NO: 19 (Thy14)

CACTTGAAATTTTNGTTAGGNCCCTTTGGGNTTCCCTTNTTCTTGTTNNT
TAANNNTGGTTNNTGCAGCTTGTCCTTTTGGCCCAACATAGGNCCTAATT
20 TCAATGGAAGTGTAGTTTTNCTCTGGGGATTCTTTAACTTTAGAGCCAT
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GTGAAAAGCTCCTTGAAAATCCAGGCGGGTATGGAAGGTGCTGCTACCCA
TATCTTTTTGACTTTCTTTGTTTTCATGACTTTAACTTCATGGCATCTCC
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25 ATAAGTACTGAGCATGAAGTACTTGTCTGCCCCCTCATTTCAAGGCCAGAG
TTATTTTCTATTTATGTATTAGTCTAGGCTGATCTTTTAGGGCACAATAG
AAACCATGGGGCGTGGAGCATGAGTTGTGAATGGCAGGGATCATTTCTGGG
TAAAAAAACCTAGAATCATTTCTGATGTGCAACATTGTCAAGTGAAGAA
GCTAACAGTTCAACTACCGAGATTATTTGATAACCTGGGTTTTCTCATTC
30 ATCCATCAAGCACCATCAACCAGTCAGCCATTATTATTTATATATGTATT
ACCAAAAGCAGTCTATCTGCCTGTGACCTCCAATGTACACTGCCAAACAC
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ATCTCCCCTTTTTCAGCCATTTCAACAACTACTCTTTGGAGCTCTGAGAT
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5

SEQ ID NO: 20 (Thy15)

GGCGGCTTTGTNGCAGNNAAGGCNGGNTNNCNAGGGATNGTTNGGACAN
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10 ACCCAAGCCAATCCAAGGTTTTNANCACGGNTGAAATTTGGAAACCNGTT
NCTAAATNCAGGTGCGGATGTGCAGGAGAAAAAATTACCAACCNCAAGGA
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15 CCATCNTTCAGGAAGAACTTGANTACATATCAAGGCAGAAGGTAAGTCA
CGAGAGANTGCAACGGATGCAATTTCCAGGCTGTGCTGTGGACTTCTTCC
AGCAGGTTTGAAGATTTGGATATTGTAACTGTGAGATCAGTGGCATTTT
TTAAATCCTTAAATGTANTTAAGATCATAAAAACATGCATCATTTCATACA
CTAGTGGGGTGGATTATTTGTGTCNTGCCTAAGTTATTTTTTTAACATTC
20 CTTTATTTCCGATTTTCATGTTTGTGTGCATTTGAGTATGTGCTGAGAAC
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ATATCAAAAATTCTAACCTGTTTACATTGTTTTTCATGTTTCATGTTTCCTAT
GTTATTAAATATTTATTTTGTAAAAA

25

SEQ ID NO: 21

gi|2723456|dbj|D30612|D30612 Homo sapiens mRNA for repressor protein
, partial cds

30

ACCCACGCGTCCGGCCGCGAAGGGGACTGTTTGCTCCTACGGGCTGTAGATGGAGCTGTCCGGCCCCGG
AGAGGGGAAGGCGCCTGGAAAACGTTCTTCTTCTCCCTGGCCGACCCGAGCGGGGAACAGCACTCCCAG
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AGCTGGAGCTGGGCCAGGCTCTGCCCCGAGCAGGTCTGCCACCAGGAGCCGGCGCTGCGCGGGGAAA
TGGCCGAGGGAATGCCGCCATGCAGGCTCAAGAATGGGACATGGACGCCCGCGGCCAATGCCTTTTCA
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35 GCAGAGATCTCACTCTGGACTGTGGTGGCTGCCATTGAGGCTGTGGAGAGGAAGGTGGATGCCAGGCCA
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CGTGGAAATTTGGGAACCATGGAGAGCAAGTGGGCCGTGCTGGGGACCCTGCTGCAGGAGTACGGGCTG
CTGCAGAGGCGGCTGGAGAACTTGGAGAACTTGCTGCGCAACAGGAACTTCTGGGTCTGCGGCTGCCCC
CGGGCAGCAAGGGGAGGCCCCAAGGTTCCAGTGACTTTTGTGACATTGCTGTGTACTTCTCCGAAGA
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5 CTCATGTCCCTGGACGCGGAGGCTCAGTCCCCAAGCCAGATGCTCCAGTCCAGGCTGAGCCCAGGGAAG
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10 TGTCCTGGATTAACAGGAGGAGCATCAGTGCCTGTGGGATCAGCAGGATTTGGCAGACAGAGATATTCC
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15 AGCCGAGGGCTGCTGGACGACGGTTTCCAGGTGCTGCCCGGGAGCGTGGCTCCGGCGAGGCGCGCCCGG
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20 CCTCATCCGCCACCAGATGACGCACCGCGCGAGCGGCCCTACAAGTGTCTCGAGTGC GAGAAGACCTAC
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35 CGCCCCAGGTTGTACATTAGAGGGCTCTTTCTCCATGGGAGCTCCTGGTGCCGCTTCGGCCCCAGCCT
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40 TGGATACAGACCTGCTGTGCTCCACACCTGCAGGCGCTCGGGAAGCGCCAAAGGATTCCCCCTCAC
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WO 00/50595

PCT/US00/04929

CATGGCCTGGCACC GGGTGGGGTGGTATGCCCCCTGTTTGTGTCAAAAATGACTTTCCTGCCCTTGCC
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CCTGCTTCGGCCCTCGCCCTCATCTACGCTGCTCCGCTTTCCTCAGACCCCTTTTGGCGTGCAAAGGAA
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5 GCCTACAGTAAAGCCTCAATGAACTGG

SEQ ID NO: 22

>gi|1503985|dbj|D86956|D86956 Human mRNA for KIAA0201 gene, complete
cds

5 CTGAGGAAGTGGGACCTCCCTTTTGGGTCGGTAGTTCAGCGCCGGCGCCGGTGTGCGAGCCGCGGCAGA
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TCAGCCAGCCCGCGCTGTCCCCGGGGAGTAGGAGGCTCCTGACAGGCCGCGGCTGTCTGTGTCTCTTC
TGAGTGTGAGAGGAACGGCCAGACCCCGGGGCCGAGCAGAACGCGGCCAGGGCAGAAAGCGGCGGCAG
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10 TCGGTGGTGGGGTTGGACGTGGGCTCGCAGAGCTGCTACATCGCGGTAGCCCCGGGCCGGGGCATCGAGA
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15 AGCCATGTTGTTGACTAAGCTGAAGGAACTGCTGAAAACAGCCTCAAGAAACCAGTAACAGATTGTGTT
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25 GAAAGAATTGCCAAATCTTTGAAAAGATATTAGCACAACTCAATGCAGATGAAGCAGTAGCCAGAG
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30 TGCACAGAAAGATGGAGAAAAATCTAGAGTAAAAGTCAAAGTGCAGTCAACACCCATGGCATTTCACC
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40 GTTAAAGTTTCGGTTTCAGGAAGCTGAAGAAGGCCAAAAATGTTTGAAGAAGTAGGACAGAGGCTGCAGC
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5 GAAAAAAGTGGAGAAGTCTGTTAATGAAGTGATGGAATGGATGAATAATGTCATGAATGCTCAGGCTAAA
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10 CCCAAATATTGATAAAAAGGAAGAAGATTTAGAAGACAAAACAATTTTGGTGCTGAACCTCCACATCAG
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15 TAAGCTTTCTGTGCAGTCTCACCATTGTCATCACTGAGGATGAACTGACTTTTGTCTTTGGAGAAAA
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20 TTTTATGAGCTTTAAATAAAGTTCATCTTATGGTGTCAATTTCT

SEQ ID NO: 23

>gi|415818|emb|X65550|HSMKI67 H.sapiens mki67a mRNA (long type) for antigen of monoclonal antibody Ki-67

5 CTACCGGGCGGAGGTGAGCGGGCGCGGCTCCTCCTGCGGCGGACTTTGGGTGCGACTTGACGAGCGGT
GGTTCGACAAGTGGCCTTGCGGGCCGGATCGTCCAGTGAAGAGTTGTAAATTTGCTTCTGGCCTTCCC
CTACGGATTATACCTGGCCTTCCCCTACGGATTATACTCAACTTACTGTTTAGAAAATGTGGCCACGAG
ACGCCTGGTTACTATCAAAAGGAGCGGGTCGACGGTCCCCACTTTCCCCTGAGCCTCAGCACCTGCTTG
TTTGAAGGGGTATTGAATGTGACATCCGTATCCAGCTTCTGTGTGTCAAAAACAACATTGCAAAATTG
10 AAATCCATGAGCAGGAGGCAATATTACATAATTTAGTTCACAAATCCAACACAAGTAAATGGGTCTGT
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15 GATGACTCAAAAGACAGTGTGCTCAGGGAACAATAATGTTTCCTCAGAACATGCTGGACGTAATG
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35 AAGAGTCTTCCAGACACGAGGTCACTGAGGAATCAATGACTAACGATAAACTGCCAAAGTAGCCTG
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SEQ ID NO: 24

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5 GATTCTCCCCATTCACCCACCTTGCCAGGTGCAGGTGAGGATGGTGCACCAGACAGGGTAGCTGTCCCC
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10 CAGGGGAGGGTGTCAAGGAAGAGTGGCTCTTAGCAGAGGCACTTTGGAAGGTGTGAGGCATAAATGCTT
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SEQ ID NO: 25

>gi|29860|emb|X55039|HSCENPB Human hCENP-B gene for centromere
autoantigen B (CENP-B)

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10 CGCAAAAAAAGTGCCTTATTTTACCTTAATTAAAAAACAACAAAAACCTGGTTCTT
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SEQ ID NO: 26

>gi|1628402|emb|X98893|HSTAFII68 H.sapiens mRNA for TBP associated factor, TAFII68

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35 GTGGAIAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 27

>gi|219909|dbj|D00017|HUMLIC Homo sapiens mRNA for lipocortin II,
complete cds

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15 ACCGAGCGGAGCGTGCCCCACCTCCAGAAAGTATTTGATAGGTACAAGAGTTACAGCCCTTATGACATGT
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SEQ ID NO: 28

>gi|37173|emb|X05615|HSTHYRR Human mRNA for thyroglobulin

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30 TTGGGAGTTCTCAGGACGACGGGCTCATCAACAGAGCAAAGGCTGTGAAGCAATTTGAGGAAAGTCAGG
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CGCGTCGAGGCTGCTGCTACATGGTATTACTCTCTGGAGCACTCCACGGATGACTATGCCTCCTTCTCCC
GGGCTCTGGAGAATGCCACCCGGGACTACTTTATCATCTGCCCTATAATCGACATGGCCAGTGCCTGGGC
AAAGAGGGCCCGAGGAAACGTCTTCATGTACCATGCTCCTGAAAACACGGCCATGGCAGCCTGGAGCTG
35 CTGGCGGATGTTCAAGTTTGCTTGGGGCTTCCCTTCTACCCAGCCTACGAGGGGCAAGTTTCTCTGAGG
AGAAGAGCCTGTGCTGAAAATCATGCAGTACTTTTCCCACTTCATCAGATCAGGAAATCCCAACTACCC
TTATGAGTTCTCACGAAAGTACCCACATTTGCAACCCCTGGCCTGACTTTGTACCCCGTGGTGGGA
GAGAACTACAAGGAGTTCACTGAGCTGCTCCCAATCGACAGGGCCTGAAGAAAGCCGACTGCTCCTCT
GGTCCAAGTACATCTCGTCTCTGAAGACATCTGCAGATGGAGCCAAGGGCGGGCAGTCAGCAGAGAGTGA
40 AGAGGAGGAGTTGACGGCTGGATCTGGGCTAAGAGAAGATCTCCTAAGCCTCCAGGAACCAGGCTCTAAG
ACCTACAGCAAGTGACCAGCCCTTGAGCTCCCAAAAACCTCACCCGAGGCTGCCCACTATGGTCATCTT

TTTCTCTAAATAGTTACTTACCTTCAATAAAGTATCTACATGCGGTG

SEQ ID NO: 29

5 >gi|339688|gb|M17733|HUMTHYB4 Human thymosin beta-4 mRNA, complete cds
ACAACTCGGTGGTGGCCACTGCGCAGACCAGACTTCGCTCGTACTCGTGCGCCTCGCTTCGCTTTTCCTC
CGCAACCATGTCTGACAAACCCGATATGGCTGAGATCGAGAAATTCGATAAGTCGAACTGAAGAAGACA
GAGACGCAAGAGAAAAATCCACTGCCTTCCAAAGAAACGATTGAACAGGAGAAGCAAGCAGGCGAATCGT
10 AATGAGGCGTGCGCCGCAATATGCACTGTACATTCCACAAGCATTGCCCTTCTTATTTTACTTCTTTTAG
CTGTTTAACTTTGTAAGATGCAAAGAGGTGGATCAAGTTTAAATGACTGTGCTGCCCTTTCACATCAA
AGAACTACTGACAACGAAGGCCGCGCTGCCTTTCCCATCTGTCTATCTATCTGGCTGGCAGGGAAGGAAA
GAACTTGCATGTTGGTGAAGGAAGAAGTGGGGTGGGAAGTGGGGTGGGACGACAGTGAAATCTAGAGT
15 AAAACCAAGCTGGCCCAAGTGTCTGCAGGTGTAATGCAGTTTAAATCAGAGTGCCATTTTTTTTT

SEQ ID NO: 30

20 >gi|1743866|gb|U70063|HSU70063 Human acid ceramidase mRNA, complete
cds
GGCACGAGGCTAGAGCGATGCCGGGCCGGAGTTGCGTCGCCTTAGTCCTCCTGGCTGCCGCCGTCAGCTG
TGCCGTCGCGCAGCACGCGCCGCGGTGGACAGGACTGCAGAAAATCAACCTATCCTCCTTCAGGACCA
ACGTACAGAGGTGCAGTTCATGGTACACCATAAATCTTGACTTACCACCCTACAAAAGATGGCATGAAT
TGATGCTTGACAAGGCACCAATGCTAAAGGTTATAGTGAATCTCTGAAGAATATGATAAATACATTCGT
25 GCCAAGTGGAAAAGTTATGCAGGTGGTGGATGAAAAATGCGCTGGCCTACTTGGCAACTTTCCTGGCCCT
TTTGAAGAGGAAATGAAGGGTATTGCCGCTGTTACTGATATACCTTTAGGAGAGATTATTTTCATTCAATA
TTTTTTATGAATTATTTACCATTTGTAAGTACCAATAGTACGAGAAGACAAAAAGGTCATCTAATACATGG
GAGAAACATGGATTTTGGAGTATTCTTGGGTGGAACATAAATAATGATACCTGGGTACATAACTGAGCAA
CTAAAACCTTTAACAGTGAATTTGGATTTCCAAAGAAACAACAAAACCTGTCTTCAAGGCTTCAAGCTTTG
30 CTGGCTATGTGGGCATGTTAACAGGATTCAAACCAGGACTGTTTCAAGTCTTACACTGAATGAACGTTTCAG
TATAAATGGTGGTTATCTGGGTATTCTAGAATGGATTCTGGGAAAGAAAGATGCCATGTGGATAGGGTTC
CTCACTAGAACAGTTCTGGAAAATAGCACAAAGTTATGAAGAAGCCAAGAATTTATTGACCAAGACCAAGA
TATTGGCCCCAGCCTACTTTATCCTGGGAGGCAACCAGTCTGGGGAAGGTTGTGTGATTACACGAGACAG
AAAGGAATCATTGGATGTATATGAACTCGATGCTAAGCAGGGTAGATGGTATGTGGTACAAACAAATTAT
35 GACCGTTGGAAACATCCCTTCTTCTTGATGATCGCAGAACGCCTGCAAAGATGTGTCTGAACCGCACCA
GCCAAGAGAAATATCTCATTTGAAACCATGTATGATGTCCTGTCAACAAAACCTGTCTCAACAAGCTGAC
CGTATACACAACCTTGATAGATGTTACCAAAGGTCAATTCGAAACTTACCTGCGGGACTGCCCTGACCCCT
TGTATAGGTTGGTGAGCACACGTCTGGCCTACAGAATGCGGCCTCTGAGACATGAAGACACCATCTCCAT
GTGACCGAACACTGCAGCTGTCTGACCTTCCAAAGACTAAGACTCGCGGCAGGTTCTCTTTGAGTCAATA
40 GCTTGTCTTCGTCCATCTGTTGACAAATGACAGATCTTTTTTTTTTTTCCCCCTATCAGTTGATTTTTCTT
ATTTACAGATAACTTCTTTAGGGGAAGTAAACAGTCATCTAGAATTCAGTGAGTTTTGTTTCACTTTGA

5 CATTGGGGATCTGGTGGGCAGTCGAACCATGGTGAACCTCCCTCCGTGGAATAAATGGAGATTCAGCG
TGGGTGTTGAATCCAGCACGTCTGTGTGAGTAACGGGACAGTAAACACTCCACATTCTTCAGTTTTTCAC
TTCTACCTACATATTTGTATGTTTTCTGTATAACAGCCTTTTCCTTCTGGTTCTAACTGCTGTAAAAAT
TAATATATCATTATCTTTGCTGTTATTGACAGCGATATTATTTTATTACATATCATTAGAGGGATGAGAC
AGACATTACCTGTATATTTCTTTTAATGGGCACAAAATGGGCCCTTGCCTCTAAATAGCACTTTTTGGG
GTTCAAGAAGTAATCAGTATGCAAAGCAATCTTTTATACAATAATTGAAGTGTTCCCTTTTTTCATAATTA
CTCTACTTCCCAGTAACCCTAAGGAAGTTGCTAACTTAAAAAACTGCATCCCACGTTCTGTAAATTTAGT
AAATAACAAGTCAAAGACTTGTGAAAAATAGGAAGTGAACCCATATTTTAAATTCATAAGTAGCATT
10 GATGTAATAAACAGGTTTTTAGTTTGTCTTCAGATTGATAGGGAGTTTAAAGAAATTTTAGTAGTTAC
TAAATTTATGTTACTGTATTTTTCAGAAATCAAAGTCTTATGAAAAGTACTAATAGAACTTGTTAACCT
TTCTAACCTTCACGATTAAGTGTGAAATGTACGTCATTTGTGCAAGACCGTTTGCCACTTCATTTGTA
TAATCACAGTTGTGTTCTGACACTCAATAAACAGTCACTGGAAAGAGTGCCAGTCAGCAGTCATGCACG
CTGATAAAAAAAAAAAAAAAAAA

15

SEQ ID NO:31 -- Oligo N1, Ki67 sense, Nhe, 6His, 5610:
ATTGCTAGCCACCACCACCACCACAACTGGACCCAGCAGCAAGTGTAAC

20 SEQ ID NO: 32 -- Oligo N2, Ki67 antisense, EcoRI, 6420:
CGGGAATTCCTATAGAGCCTCAGCCTTTTCCTTAGG